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PROTEIN-PROTEIN INTERACTIONS Between Shigella flexneri polypeptides And Mammalian Polypeptides

PRIORITY

[0001] This application claims priority on the basis of United States Provisional Application No. 60/261,130, filed January 12, 2001, the contents of which are hereby incorporated by reference.

BACKGROUND OF THE INVENTION

[0002] Most biological processes involve specific protein-protein interactions. Protein-protein interactions enable two or more proteins to associate. A large number of non-covalent bonds form between the proteins when two protein surfaces are precisely matched. These bonds account for the specificity of recognition. Thus, protein-protein interactions are involved, for example, in the assembly of enzyme subunits, in antibody-antigen recognition, in the formation of biochemical complexes, in the correct folding of proteins, in the metabolism of proteins, in the transport of proteins, in the localization of proteins, in protein turnover, in first translation modifications, in the core structures of viruses and in signal transduction.

[0003] General methodologies to identify interacting proteins or to study these interactions have been developed. Among these methods are the two-hybrid system originally developed by Fields and co-workers and described, for example, in U.S. Patent Nos. 5,283,173, 5,468,614 and 5,667,973, which are hereby incorporated by reference.

[0004] The earliest and simplest two-hybrid system, which acted as basis for development of other versions, is an *in vivo* assay between two specifically constructed proteins. The first protein, known in the art as the "bait protein" is a chimeric protein which binds to a site on DNA upstream of a reporter gene by means of a DNA-binding domain or BD. Commonly, the binding domain is the DNA-binding domain from either Gal4 or native *E. coli* LexA and the sites placed upstream of the reporter are Gal4 binding sites or LexA operators, respectively.

[0005] The second protein is also a chimeric protein known as the "prey" in the art. This second chimeric protein carries an activation domain or AD. This activation domain is typically derived from Gal4, from VP16 or from B42.

[0006] Besides the two hybrid systems, other improved systems have been developed to detected protein-protein interactions. For example, a two-hybrid plus one system was developed that allows the use of two proteins as bait to screen available cDNA libraries to detect a third partner. This method permits the detection between proteins that are part of a larger protein complex such as the RNA polymerase II holoenzyme and the TFIIH or TFIID complexes. Therefore, this method, in general, permits the detection of ternary complex

formation as well as inhibitors preventing the interaction between the two previously defined fused proteins.

[0007] Another advantage of the two-hybrid plus one system is that it allows or prevents the formation of the transcriptional activator since the third partner can be expressed from a conditional promoter such as the methionine-repressed Met25 promoter which is positively regulated in medium lacking methionine. The presence of the methionine-regulated promoter provides an excellent control to evaluate the activation or inhibition properties of the third partner due to its "on" and "off" switch for the formation of the transcriptional activator. The three-hybrid method is described, for example in Tirode et al., *The Journal of Biological Chemistry*, **272**, No. 37 pp. 22995-22999 (1997). incorporated herein by reference.

[0008] Besides the two and two-hybrid plus one systems, yet another variant is that described in Vidal et al, *Proc. Natl. Sci. 93* pgs. 10315-10320 called the reverse two- and one-hybrid systems where a collection of molecules can be screened that inhibit a specific protein-protein or protein/DNA interactions, respectively.

[0009] A summary of the available methodologies for detecting protein-protein interactions is described in Vidal and Legrain, *Nucleic Acids Research* Vol. 27, No. 4 pgs.919-929 (1999) and Legrain and Selig, FEBS Letters 480 pgs. 32-36 (2000) which references are incorporated herein by reference.

[0010] However, the above conventionally used approaches and especially the commonly used two-hybrid methods have their drawbacks. For example, it is known in the art that, more often than not, false positives and false negatives exist in the screening method. In fact, a doctrine has been developed in this field for interpreting the results and in common practice an additional technique such as co-immunoprecipitation or gradient sedimentation of the putative interactors from the appropriate cell or tissue type are generally performed. The methods used for interpreting the results are described by Brent and Finley, Jr. in *Ann. Rev. Genet., 31 pgs. 663-704 (1997).* Thus, the data interpretation is very questionable using the conventional systems.

[0011] One method to overcome the difficulties encountered with the methods in the prior art is described in WO 99/42612, incorporated herein by reference. This method is similar to the two-hybrid system described in the prior art in that it also uses bait and prey polypeptides. However, the difference with this method is that a step of mating at least one first haploid recombinant yeast cell containing the prey polypeptide to be assayed with a second haploid recombinant yeast cell containing the bait polynucleotide is performed. Of course the person skilled in the art would appreciate that either the first recombinant yeast cell or the second recombinant yeast cell also contains at least one detectable reporter gene that is activated by a polypeptide including a transcriptional activation domain.

[0012] The method described in WO 99/42612 permits the screening of more prey polynucleotides with a given bait polynucleotide in a single step than in the prior art systems due to the cell to cell mating strategy between haploid yeast cells. Furthermore, this method is more thorough and reproducible, as well as sensitive. Thus, the presence of false negatives and/or false positives is extremely minimal as compared to the conventional prior art methods.

[0013] The genus *Shigella* includes four species (major serogroups): *S. dysenteriae* (Grp. A), *S. flexneri* (Grp. B), *S. boydii* (Grp. C) and *S. sonnei* (Grp. D) as classified in Bergey's Manual for Systematic Bacteriology (N. R. Krieg, ed., pp. 423-427 (1984)). The genera *Shigella* and *Escherichia* are phylogenetically closely related. Brenner and others have suggested that the two are more correctly considered sibling species based on DNA/DNA reassociation studies (D. J. Brenner et al., International J. Systematic Bacteriology, 23:1-7 (1973)). These studies showed that *Shigella* species are on average 80-89% related to *E. coli* at the DNA level. Also, the degree of relatedness between *Shigella* species is on average 80-89%.

[0014] The genus *Shigella* is pathogenic in humans; it causes bacillary dysentery at levels of infection of 10 to 100 organisms.

[0015] Shigellosis or bacillary dysentery is a disease that is endemic throughout the world. The disease presents a particularly serious public health problem in tropical regions and developing countries where *Shigella dysenteriae* and *S. flexneri* predominate. In industrialized countries, the principal etiologic agent is *S. sonnei* although sporadic cases of shigellosis are encountered due to *S. flexneri*, *S. boydii* and certain entero-invasive *Escherichia coli*.

[0016] The primary step in the pathogenesis of bacillary dysentery is invasion of the human colonic mucosa by *Shigella* (Labrec, E. H., H. Schneider, T. J. Magnani, and S. B. Formal. 1964. Epithelial cell penetration as an essential step in the pathogenesis of bacillary dysentery. J. Bacteriol. 88:1503). Mucosal invasion encompasses several steps which include penetration of the bacteria into epithelial cells, intracellular multiplication, killing of host cells, and final spreading to adjacent cells and to connective tissue (Formal, S. B., T. L. Hale, and P. J. Sansonetti. 1983. Invasive enteric pathogens. Rev. Infect. Dis. 5:S702, Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Takeuchi, A., H. Spring, E. H. LaBrec, and S. B. Formal. 1965. Experimental acute colitis in the Rhesus monkey following peroral infection with Shigella flexneri. Am. J. Pathol. 52:503, Takeuchi, A. 1967. Electron microscope studies of experimental Salmonella infection. I. Penetration into cells of the intestinal epithelium by Salmonella typhimurium. Am. J. Pathol. 47:1011). The overall process which is usually

limited to the mucosal surface leads to a strong inflammatory reaction which is responsible for abscesses and ulcerations (Labrec, E. H., H. Schneider, T. J. Magnani, and S. B. Formal. 1964. Epithelial cell penetration as an essential step in the pathogenesis of bacillary dysentery. J. Bacteriol. 88:1503., Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Takeuchi, A., H. Spring, E. H. LaBrec, and S. B. Formal. 1965. Experimental acute colitis in the Rhesus monkey following peroral infection with Shigella flexneri. Am. J. Pathol. 52:503).

[0017] Even though dysentery is characteristic of shigellosis, it may be preceded by watery diarrhea. Diarrhea appears to be the result of disturbances in colonic reabsorption and increased jejunal secretion whereas dysentery is a purely colonic process (Kinsey, M. D., S. B. Formal, G. J. Dammin, and R. A. Giannella. 1976. Fluid and electrolyte transport in Rhesus monkeys challenged intraceacally with Shigella flexneri 2a. Infect. Immun. 14:368). These include toxic megacolon, leukemoid reactions and hemolytic-uremic syndrome ("HUS"). The latter is a major cause of mortality from shigellosis in developing areas (Gianantonio, C., H. Vitacco, F. Mendilaharzu, A. Rutty, and J. Mendilaharzu. 1964. The hemolytic-uremic syndrome. J. Pediatr. 64:478, Koster, F., J. Levin, L. Walker, K. S. K. Tung, R. H. Gilman, M. M. Rajaman, M. A. Majid, S. Islam, and R. C. Williams Jr. 1977. Hemolyticuremic syndrome after shigellosis. Relation to endotoxin and circulating immune complexes. N. Engl. J. Med. 298:927).

[0018] The role of Shiga-toxin produced at high level by S. dysenteriae 1 (Conradi, H., 1903. Ueber loshlishe, durch aseptische Autolyse, erhaltene Giftstoffe von Ruhr--un Typhus bazillen. Dtsch. Med. Wochenschr. 29:26) and Shiga-like toxins ("SLT") produced at low level by S. flexneri and S. sonnei (Keusch, G. T., and M. Jacewicz, 1977. The pathogenesis of Shigella diarrhea. VI. Toxin and antitoxin in Shigella flexneri and Shigella sonnei infections in humans. J. Infect. Dis. 135:552) in the four major stages of shigellosis (i.e., invasion of individual epithelial cells, tissue invasion, diarrhea and systemic symptoms) is not well understood. For review see O'Brien and Holmes (O'Brien, A. D., and R. K. Holmes. 1987. Shiga and Shiga-like toxins. Microbiol. Rev. 51:206). Plasmids of 180-220 kilobases ("kb") are essential in all Shigella species for invasion of individual epithelial cells (Rout, W. R., S. B. Formal, R. A. Giannella, and G. J. Dammin. 1975. The pathophysiology of Shigella diarrhea in the Rhesus monkey; intestinal transport, morphology and bacteriological studies. Gastroenterology 68:270, Sansonetti, P. J., D. J. Kopecko, and S. B. Formal. 1981. Shiqella sonnei plasmids: evidence that a large plasmid is necessary for virulence. Infect. Immun. 34:75, Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal. 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392). This

includes entry, intracellular multiplication and early killing of host cells (Clerc, P., A. Ryter, J. Mounier, and P. J. Sansonetti. 1987. Plasmid-mediated early killing of eucaryotic cells by Shigella flexneri as studied by infection of J774 macrophages. Infect. Immun. 55:521, Clerc, P., and P. J. Sansonetti. 1987. Entry of *Shigella flexneri* into HeLa cells: Evidence for directed phagocytosis involving actin polymerization and myosin accumulation. Infect. Immun. 55:2681). The role of Shiga-toxin and SLT at this stage is unclear.

[0019] Recent evidence indicates that Shiga-toxin is cytotoxic for primary cultures of human colonic cells (Moyer, M. P., P. S. Dixon, S. W. Rothman, and J. E. Brown. 1987. Cytotoxicity of Shiga toxin for human colonic and ileal epithelial cells. Infect. Immun. 55:1533). Tissue invasion requires additional chromosomally encoded products among which are smooth lipopolysaccharides ("LPS") (Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal. 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392), the non-characterized product of the Kcp locus, and aerobactin. A region of the S. flexneri chromosome necessary for fluid production in rabbit ileal loops has been localized to the rha-mt1 regions and near the lysine decarboxylase locus (Sansonetti, P. J., T. L. Hale, G. I. Dammin, C. Kapper, H. H. Collins Jr., and S. B. Formal. 1983. Alterations in the pathogenesis of Escherichia coli K12 after transfer of plasmids and chromosomal genes from Shigella flexneri. Infect. Immun. 39:1392). However, no evidence has been adduced to show that the ability to cause fluid accumulation is due to the SLT of S. flexneri. Thus, the role of Shiga-toxin in causing the systemic complications of shigellosis is still hypothetical. However, Shiga-toxin can mediate vascular damage since capillary lesions observed in HUS resemble those observed in cerebral vessels of animals injected with this toxin (Bridgewater, F. A. I., R. S. Morgan, K. E. K. Rowson, and G. P. Wright, 1955, the neurotoxin of Shigella shigae. Morphological and functional lesions produced in the central nervous system of rabbits. Br. J. Exp. Pathol. 36: 447, Cavanagh, J. B., J. G. Howard, and J. L. Whitby. 1956. The neurotoxin of Shigella shigae. A comparative study of the effects produced in various laboratory animals. Br. J. Exp. Med. 37:272).

[0020] As described before, the genera of *Shigella* and *Escherichia* are phylogenetically closely related. Furthermore, the pathogenesis of enteroinvasive *E. coli* is very similar to that of *Shigella*. In both, dysentery results from invasion of the colonic epithelial cells followed by intracellular multiplication which leads to bloody, mucous discharge with scanty diarrhea.

[0021] Pathogenic *E. coli* serotypes are collectively referred to as Enterovirulent *E. coli* (EVEC) (J. R. Lupski, et al., J. Infectious Diseases, 157:1120-1123 (1988); M. M. Levine, J. Infectious Diseases, 155:377-389 (1987); M. A. Karmali, Clinical Microbiology Reviews, 2:15-38 (1989)). This group includes at least 5 subclasses of *E. coli*, each having a

characteristic pathogenesis pathway resulting in diarrheal disease. The subclasses include Enterotoxigenic *E. coli* (ETEC), Verotoxin-Producing *E. coli* (VTEC), Enteropathogenic *E. coli* (EPEC), Enteroadherent E. coli (EAEC) and Enteroinvasive E. coli (EIEC). The VTEC include Enterohemorrhagic *E. coli* (EHEC) since these produce verotoxins.

[0022] Thus, detection of *Shigella* and EIEC is important in various medical contexts. For example, the presence of either *Shigella* or EIEC in stool samples is indicative of gastroenteritis, and the ability to screen for their presence is useful in treating and controlling that disease. Detection of *Shigella* or EIEC in any possible transmission vehicle such as food is also important to avoid spread of gastroenteritis.

[0023] That is why there is a great need to construct Protein Interaction Map between *Shigella* polypeptides and human polypeptides in order to understand mechanisms of *Shigella* pathogenesis and to identify drug target to treat *Shigella* associated diseases and *Shigella* detection means.

SUMMARY OF THE PRESENT INVENTION

[0024] Thus, it is an object of the present invention to identify protein-protein interactions between *Shigella* polypeptides and mammalian, preferably human, polypeptides.

[0025] It is another object of the present invention to identify protein-protein interactions between *Shigella* polypeptides and mammalian, preferably human, polypeptides for the development of more effective and better targeted therapeutic applications.

[0026] It is yet another object of the present invention to identify complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Shigella* genus and polypeptides and fragments of the polypeptides of mammals, preferably human.

[0027] It is yet another object of the present invention to identify antibodies to these complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Shigella* genus and mammals, preferably human, including polyclonal, as well as monoclonal antibodies that are used for detection.

[0028] It is still another object of the present invention to identify selected interacting domains of the polypeptides, called SID® polypeptides.

[0029] It is still another object of the present invention to identify selected interacting domains of the polynucleotides, called SID® polynucleotides.

[0030] It is another object of the present invention to generate protein-protein interactions maps called PIM®s.

[0031] It is yet another object of the present invention to provide a method for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions between *Shigella* polypeptides and mammalian, preferably human, polypeptides.

[0032] It is another object to administer the nucleic acids of the present invention via gene therapy.

[0033] It is yet another object of the present invention to provide protein chips or protein microarrays.

[0034] It is yet another object of he present invention to provide a report in, for example paper, electronic and/or digital forms, concerning the protein-protein interactions, the modulating compounds and the like as well as a PIM®.

[0035] Thus the present invention, in one aspect thereof, relates to a protein complex between a *Shigella* polypeptide and a mammalian polypeptide. In another embodiment, the Shigella and the mammalian polypeptides are polypeptides set forth on columns 1 and 3 respectively of Table II.

[0036] Furthermore, the present invention provides SID® polynucleotides and SID® polypeptides of Table III, as well as a PIM® between *Shigella* polypeptides and mammalian, preferably human, polypeptides.

[0037] The present invention also provides antibodies to the protein-protein complexes between *Shigella* polypeptides and mammal, preferably human, polypeptides.

[0038] In another embodiment the present invention provides a method for screening drugs for agents that modulate the protein-protein interactions and pharmaceutical compositions that are capable of modulating protein-protein interactions.

[0039] In another embodiment the present invention provides protein chips or protein microarrays.

[0040] In yet another embodiment the present invention provides a report in, for example, paper, electronic and/or digital forms.

BRIEF DESCRIPTION OF THE DRAWINGS

- [0041] Fig. 1 is a schematic representation of the pB1 plasmid.
- [0042] Fig. 2 is a schematic representation of the pB5 plasmid.
- [0043] Fig. 3 is a schematic representation of the pB6 plasmid.
- [0044] Fig. 4 is a schematic representation of the pB13 plasmid.
- [0045] Fig. 5 is a schematic representation of the pB14 plasmid.
- [0046] Fig. 6 is a schematic representation of the pB20 plasmid.
- [0047] Fig. 7 is a schematic representation of the pP1 plasmid.
- [0048] Fig. 8 is a schematic representation of the pP2 plasmid.
- [0049] Fig. 9 is a schematic representation of the pP3 plasmid.
- [0050] Fig. 10 is a schematic representation of the pP6 plasmid.
- [0051] Fig. 11 is a schematic representation of the pP7 plasmid.
- [0052] Fig. 12 is a schematic representation of vectors expressing the T25 fragment.
- [0053] Fig. 13 is a schematic representation of vectors expressing the T18 fragment.

[0054] Fig. 14 is a schematic representation of various vectors of pCmAHL1, pT25 and pT18.

[0055] Fig. 15 is a schematic representation of identification of SID®. In this figure the "Full-length prey protein" is the Open Reading Frame (ORF) or coding sequence (CDS) where the identified prey polypeptides are included. The Selected Interaction Domain (SID®) is determined by the commonly shared polypeptide domain of every selected prey fragment.

[0056] Fig. 16 is a protein map (PIM®).

DETAILED DESCRIPTION OF THE INVENTION

[0057] As used herein the terms "polynucleotides", "nucleic acids" and "oligonucleotides" are used interchangeably and include, but are not limited to RNA, DNA, RNA/DNA sequences of more than one nucleotide in either single chain or duplex form. The polynucleotide sequences of the present invention may be prepared from any known method including, but not limited to, any synthetic method, any recombinant method, any *ex vivo* generation method and the like, as well as combinations thereof.

[0058] The term "polypeptide" means herein a polymer of amino acids having no specific length. Thus, peptides, oligopeptides and proteins are included in the definition of "polypeptide" and these terms are used interchangeably throughout the specification, as well as in the claims. The term "polypeptide" does not exclude post-translational modifications such as polypeptides having covalent attachment of glycosyl groups, aceteyl groups, phosphate groups, lipid groups and the like. Also encompassed by this definition of "polypeptide" are homologs thereof.

[0059] By the term "homologs" is meant structurally similar genes contained within a given species, orthologs are functionally equivalent genes from a given species or strain, as determined for example, in a standard complementation assay. Thus, a polypeptide of interest can be used not only as a model for identifying similiar genes in given strains, but also to identify homologs and orthologs of the polypeptide of interest in other species. The orthologs, for example, can also be identified in a conventional complementation assay. In addition or alternatively, such orthologs can be expected to exist in bacteria (or other kind of cells) in the same branch of the phylogenic tree, as set forth, for example, at ftp://ftp.cme.msu.edu/pub/rdp/SSU-rRNA/SSU/Prok.phylo.

[0060] As used herein the term "prey polynucleotide" means a chimeric polynucleotide encoding a polypeptide comprising (i) a specific domain; and (ii) a polypeptide that is to be tested for interaction with a bait polypeptide. The specific domain is preferably a transcriptional activating domain.

[0061] As used herein, a "bait polynucleotide" is a chimeric polynucleotide encoding a chimeric polypeptide comprising (i) a complementary domain; and (ii) a polypeptide that is to

be tested for interaction with at least one prey polypeptide. The complementary domain is preferably a DNA-binding domain that recognizes a binding site that is further detected and is contained in the host organism.

[0062] As used herein "complementary domain" is meant a functional constitution of the activity when bait and prey are interacting; for example, enzymatic activity.

[0063] As used herein "specific domain" is meant a functional interacting activation domain that may work through different mechanisms by interacting directly or indirectly through intermediary proteins with RNA polymerase II or III-associated proteins in the vicinity of the transcription start site.

[0064] As used herein the term "complementary" means that, for example, each base of a first polynucleotide is paired with the complementary base of a second polynucleotide whose orientation is reversed. The complementary bases are A and T (or A and U) or C and G.

[0065] The term "sequence identity" refers to the identity between two peptides or between two nucleic acids. Identity between sequences can be determined by comparing a position in each of the sequences which may be aligned for the purposes of comparison. When a position in the compared sequences is occupied by the same base or amino acid, then the sequences are identical at that position. A degree of sequence identity between nucleic acid sequences is a function of the number of identical nucleotides at positions shared by these sequences. A degree of identity between amino acid sequences is a function of the number of identical amino acid sequences that are shared between these sequences. Since two polypeptides may each (i) comprise a sequence (i.e., a portion of a complete polynucleotide sequence) that is similar between two polynucleotides, and (ii) may further comprise a sequence that is divergent between two polynucleotides, sequence identity comparisons between two or more polynucleotides over a "comparison window" refers to the conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference nucleotide sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

[0066] To determine the percent identity of two amino acids sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison. For example, gaps can be introduced in the sequence of a first amino acid sequence or a first nucleic acid sequence for optimal alignment with the second amino acid sequence or second nucleic acid sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied

by the same amino acid residue or nucleotide as the corresponding position in the second sequence, the molecules are identical at that position.

[0067] The percent identity between the two sequences is a function of the number of identical positions shared by the sequences. Hence % identity = number of identical positions / total number of overlapping positions X 100.

[0068] In this comparison the sequences can be the same length or may be different in length. Optimal alignment of sequences for determining a comparison window may be conducted by the local homology algorithm of Smith and Waterman (*J. Theor. Biol.*, 91 (2) pgs. 370-380 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Miol. Biol.*, 48(3) pgs. 443-453 (1972), by the search for similarity via the method of Pearson and Lipman, *PNAS*, *USA*, 85(5) pgs. 2444-2448 (1988) , by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetic Computer Group, 575, Science Drive, Madison, Wisconsin) or by inspection.

[0069] The best alignment (i.e., resulting in the highest percentage of identity over the comparison window) generated by the various methods is selected.

[0070] The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide by nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size) and multiplying the result by 100 to yield the percentage of sequence identity. The same process can be applied to polypeptide sequences.

[0071] The percentage of sequence identity of a nucleic acid sequence or an amino acid sequence can also be calculated using BLAST software (Version 2.06 of September 1998) with the default or user defined parameter.

[0072] The term "sequence similarity" means that amino acids can be modified while retaining the same function. It is known that amino acids are classified according to the nature of their side groups and some amino acids such as the basic amino acids can be interchanged for one another while their basic function is maintained.

[0073] The term "isolated" as used herein means that a biological material such as a nucleic acid or protein has been removed from its original environment in which it is naturally present. For example, a polynucleotide present in a plant, mammal or animal is present in its natural state and is not considered to be isolated. The same polynucleotide separated

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from the adjacent nucleic acid sequences in which it is naturally inserted in the genome of the plant or animal is considered as being "isolated."

[0074] The term "isolated" is not meant to exclude artificial or synthetic mixtures with other compounds, or the presence of impurities which do not interfere with the biological activity and which may be present, for example, due to incomplete purification, addition of stabilizers or mixtures with pharmaceutically acceptable excipients and the like.

[0075] "Isolated polypeptide" or "isolated protein" as used herein means a polypeptide or protein which is substantially free of those compounds that are normally associated with the polypeptide or protein in a naturally state such as other proteins or polypeptides, nucleic acids, carbohydrates, lipids and the like.

[0076] The term "purified" as used herein means at least one order of magnitude of purification is achieved, preferably two or three orders of magnitude, most preferably four or five orders of magnitude of purification of the starting material or of the natural material. Thus, the term "purified" as utilized herein does not mean that the material is 100% purified and thus excludes any other material.

[0077] The term "variants" when referring to, for example, polynucleotides encoding a polypeptide variant of a given reference polypeptide are polynucleotides that differ from the reference polypeptide but generally maintain their functional characteristics of the reference polypeptide. A variant of a polynucleotide may be a naturally occurring allelic variant or it may be a variant that is known naturally not to occur. Such non-naturally occurring variants of the reference polynucleotide can be made by, for example, mutagenesis techniques, including those mutagenesis techniques that are applied to polynucleotides, cells or organisms.

[0078] Generally, differences are limited so that the nucleotide sequences of the reference and variant are closely similar overall and, in many regions identical.

[0079] Variants of polynucleotides according to the present invention include, but are not limited to, nucleotide sequences which are at least 95% identical after alignment to the reference polynucleotide encoding the reference polypeptide. These variants can also have 96%, 97%, 98% and 99.999% sequence identity to the reference polynucleotide.

[0080] Nucleotide changes present in a variant polynucleotide may be silent, which means that these changes do not alter the amino acid sequences encoded by the reference polynucleotide.

[0081] Substitutions, additions and/or deletions can involve one or more nucleic acids. Alterations can produce conservative or non-conservative amino acid substitutions, deletions and/or additions.

[0082] Variants of a prey or a SID® polypeptide encoded by a variant polynucleotide can possess a higher affinity of binding and/or a higher specificity of binding to its protein or

polypeptide counterpart, against which it has been initially selected. In another context, variants can also loose their ability to bind to their protein or polypeptide counterpart.

[0083] By "anabolic pathway" is meant a reaction or series of reactions in a metabolic pathway that synthesize complex molecules from simpler ones, usually requiring the input of energy. An anabolic pathway is the opposite of a catabolic pathway.

[0084] As used herein, a "catabolic pathway" is a series of reactions in a metabolic pathway that break down complex compounds into simpler ones, usually releasing energy in the process. A catabolic pathway is the opposite of an anabolic pathway.

[0085] As used herein, "drug metabolism" is meant the study of how drugs are processed and broken down by the body. Drug metabolism can involve the study of enzymes that break down drugs, the study of how different drugs interact within the body and how diet and other ingested compounds affect the way the body processes drugs.

[0086] As used herein, "metabolism" means the sum of all of the enzyme-catalyzed reactions in living cells that transform organic molecules.

[0087] By "secondary metabolism" is meant pathways producing specialized metabolic products that are not found in every cell.

[0088] As used herein, "SID®" means a Selected Interacting Domain and is identified as follows: for each bait polypeptide screened, selected prey polypeptides are compared. Overlapping fragments in the same ORF or CDS define the selected interacting domain.

[0089] As used herein the term "PIM®" means a protein-protein interaction map. This map is obtained from data acquired from a number of separate screens using different bait polypeptides and is designed to map out all of the interactions between the polypeptides.

[0090] The term "affinity of binding", as used herein, can be defined as the affinity constant Ka when a given SID® polypeptide of the present invention which binds to a polypeptide and is the following mathematical relationship:

- [0091] [SID®/polypeptide complex]
- [0092] Ka = -----
- [0093] [free SID®] [free polypeptide]

[0094] wherein [free SID®], [free polypeptide] and [SID®/polypeptide complex] consist of the concentrations at equilibrium respectively of the free SID® polypeptide, of the free polypeptide onto which the SID® polypeptide binds and of the complex formed between SID® polypeptide and the polypeptide onto which said SID® polypeptide specifically binds.

[0095] The affinity of a SID® polypeptide of the present invention or a variant thereof for its polypeptide counterpart can be assessed, for example, on a Biacore™ apparatus marketed by Amersham Pharmacia Biotech Company such as described by Szabo et al *Curr*

Opin Struct Biol 5 pgs. 699-705 (1995) and by Edwards and Leartherbarrow, Anal. Biochem 246 pgs. 1-6 (1997).

[0096] As used herein the phrase "at least the same affinity" with respect to the binding affinity between a SID® polypeptide of the present invention to another polypeptide means that the Ka is identical or can be at least two-fold, at least three-fold or at least five fold greater than the Ka value of reference.

[0097] As used herein, the term "modulating compound" means a compound that inhibits or stimulates or can act on another protein which can inhibit or stimulate the protein-protein interaction of a complex of two polypeptides or the protein-protein interaction of two polypeptides.

[0098] More specifically, the present invention comprises complexes of polypeptides or polynucleotides encoding the polypeptides composed of a bait polypeptide, or a bait polynucleotide encoding a bait polypeptide and a prey polypeptide or a prey polynucleotide encoding a prey polypeptide. The prey polypeptide or prey polynucleotide encoding the prey polypeptide is capable of interacting with a bait polypeptide of interest in various hybrid systems.

[0099] As described in the Background of the present invention there are various methods known in the art to identify prey polypeptides that interact with bait polypeptides of interest. These methods, include, but are not limited to, generic two-hybrid systems as described by Fields et al in *Nature*, 340:245-246 (1989) and more specifically in U.S. Patent Nos. 5,283,173, 5,468,614 and 5,667,973, which are hereby incorporated by reference; the reverse two-hybrid system described by Vidal et al, *supra*; the two plus one hybrid method described, for example, in Tirode et al, *supra*; the yeast forward and reverse 'n'-hybrid systems as described in Vidal and Legrain, *supra*; the method described in WO 99/42612; those methods described in Legrain et al *FEBS Letters* 480 pgs. 32-36 (2000) and the like.

[0100] The present invention is not limited to the type of method utilized to detect protein-protein interactions and therefore any method known in the art and variants thereof can be used. It is however better to use the method described in WO 99/42612 or WO 00/66722, both references incorporated herein by reference due to the methods' sensitivity, reproducibility and reliability.

[0101] Protein-protein interactions can also be detected using complementation assays such as those described by Pelletier et al. at http://www.abrf.org/JBT/Articles/JBT0012/jbt0012.html, WO 00/07038 and WO98/34120.

[0102] Although the above methods are described for applications in the yeast system, the present invention is not limited to detecting protein-protein interactions using yeast, but also includes similar methods that can be used in detecting protein-protein interactions in, for example, mammalian systems as described, for example in Takacs et al., *Proc. Natl. Acad.*

Sci., USA, **90** (21):10375-79 (1993) and Vasavada et al., *Proc. Natl. Acad. Sci., USA*, 88 (23):10686-90 (1991), as well as a bacterial two-hybrid system as described in Karimova et al (1998), WO99/28746, WO 00/66722 and Legrain et al *FEBS Letters*, **480** pgs. 32-36 (2000).

[0103] The above-described methods are limited to the use of yeast, mammalian cells and *Escherichia coli* cells, the present invention is not limited in this manner. Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungus, insect, nematode and plant cells are encompassed by the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

[0104] Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61, COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

[0105] Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, (e.g., strain DH5- α), *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyce*s and *Staphylococcus*.

[0106] Further suitable cells that can be used in the present invention include yeast cells such as those of *Saccharomyces* such as *Saccharomyces cerevisiae*.

[0107] The bait polynucleotide, as well as the prey polynucleotide can be prepared according to the methods known in the art such as those described above in the publications and patents reciting the known method *per se*.

[0108] The bait polynucleotide of the present invention is obtained from *Shigella flexneri* (see Table I). The prey polynucleotide is obtained form a human placenta cDNA or variants thereof and fragments from the genome or transcriptome of human placenta ranging from about 12 to about 5,000, or about 12 to about 10,000 or from about 12 to about 20,000. The prey polynucleotide is then selected, sequenced and identified.

[0109] A human placenta cDNA prey library is prepared from global human placenta and constructed in the specially designed prey vector pP6 as shown in Figure 10 after ligation of suitable linkers such that every cDNA fragment insert is fused to a nucleotide sequence in the vector that encodes the transcription activation domain of a reporter gene. Any transcription activation domain can be used in the present invention. Examples include, but are not limited to, Gal4,YP16, B42, His and the like. Toxic reporter genes, such as CAT^R, CYH2, CYH1, URA3, bacterial and fungi toxins and the like can be used in reverse two-hybrid systems.

- [0110] The polypeptides encoded by the nucleotide inserts of the human placenta cDNA prey library thus prepared are termed "prey polypeptides" in the context of the presently described selection method of the prey polynucleotides.
- [0111] The bait polynucleotide can be inserted in bait plasmid pB6 or pB20 as illustrated in Figure 3 or 6 respectively. The bait polynucleotide insert is fused to a polynucleotide encoding the binding domain of, for example, the Gal4 DNA binding domain and the shuttle expression vector is used to transform cells. The bait polynucleotides used in the present invention are describes in Table I. As stated above, any cells can be utilized in transforming the bait and prey polynucleotides of the present invention including mammalian cells, bacterial cells, yeast cells, insect cells and the like.
- [0112] In an embodiment, the present invention identifies protein-protein interactions in yeast. In using known methods a prey positive clone is identified containing a vector which comprises a nucleic acid insert encoding a prey polypeptide which binds to a bait polypeptide of interest. The method in which protein-protein interactions are identified comprises the following steps:
- [0113] mating at least one first haploid recombinant yeast cell clone from a recombinant yeast cell clone library that has been transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant yeast cell clone transformed with a plasmid containing a bait polynucleotide encoding for the bait polypeptide;
- [0114] cultivating diploid cell clones obtained in step i) on a selective medium; and
- [0115] selecting recombinant cell clones which grow on the selective medium.
- [0116] This method may further comprise the step of:
- [0117] iv) characterizing the prey polynucleotide contained in each recombinant cell clone which is selected in step iii).
- [0118] In yet another embodiment of the present invention, in lieu of yeast, Escherichia coli is used in a bacterial two-hybrid system, which encompasses a similar principle to that described above for yeast, but does not involve mating for characterizing the prey polynucleotide.
- [0119] In yet another embodiment of the present invention, mammalian cells and a method similar to that described above for yeast for characterizing the prey polynucleotide are used.
- [0120] By performing the yeast, bacterial or mammalian two-hybrid system it is possible to identify for one particular bait an interacting prey polypeptide. The prey polypeptide that has been selected by testing the library of preys in a screen using the two-hybrid, two plus one hybrid methods and the like, encodes the polypeptide interacting with the protein of interest.

[0121] The present invention is also directed, in a general aspect, to a complex of polypeptides, polynucleotides encoding the polypeptides composed of a bait polypeptide or bait polynucleotide encoding the bait polypeptide and a prey polypeptide or prey polynucleotide encoding the prey polypeptide capable of interacting with the bait polypeptide of interest. These complexes are identified in Table II, as the bait amino acid sequences and the prey amino acid sequences, as well as the bait and prey nucleic acid sequences.

[0122] In another aspect, the present invention relates to a complex of polynucleotides consisting of a first polynucleotide, or a fragment thereof, encoding a prey polypeptide that interacts with a bait polypeptide and a second polynucleotide or a fragment thereof. This fragment has at least 12 consecutive nucleotides, but can have between 12 and 5,000 consecutive nucleotides, or between 12 and 10,000 consecutive nucleotides or between 12 and 20,000 consecutive nucleotides.

[0123] The polypeptides of column 1 and 3 from Table II according to the present invention and the complexes of these two polypeptides also form part of the present invention. More specifically, the polypeptides of SEQ ID NOS. 1 to 7 are part of the present invention and their complexes with the polypeptides of Column 3, Table II.

[0124] In yet another embodiment, the present invention relates to an isolated complex of at least two polypeptides encoded by two polynucleotides wherein said two polypeptides are associated in the complex by affinity binding and are depicted in columns 1 and 3 of Table II.

[0125] In yet another embodiment, the present invention relates to an isolated complex comprising at least a polypeptide as described in column 1 of Table II and a polypeptide as described in column 3 of Table II. The present invention is not limited to these polypeptide complexes alone but also includes the isolated complex of the two polypeptides in which fragments and/or homologous polypeptides exhibiting at least 95% sequence identity, as well as from 96% sequence identity to 99.999% sequence identity.

[0126] Also encompassed in another embodiment of the present invention is an isolated complex in which SID® of the prey polypeptides encoded by SEQ ID Nos. 15 to 215 in Table III form the isolated complex.

[0127] Besides the isolated complexes described above, nucleic acids coding for a Selected Interacting Domain (SID®) polypeptide or a variant thereof or any of the nucleic acids set forth in Table III can be inserted into an expression vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Such transcription elements include a regulatory region and a promoter. Thus, the nucleic acid which may encode a marker compound of the present invention is operably linked to a promoter in the expression vector. The expression vector may also include a replication origin.

[0128] A wide variety of host/expression vector combinations are employed in expressing the nucleic acids of the present invention. Useful expression vectors that can be used include, for example, segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include, but are not limited to, derivatives of SV40 and pcDNA and known bacterial plasmids such as col EI, pCR1, pBR322, pMaI-C2, pET, pGEX as described by Smith et al [need cite 1988], pMB9 and derivatives thereof, plasmids such as RP4, phage DNAs such as the numerous derivatives of phage I such as NM989, as well as other phage DNA such as M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 micron plasmid or derivatives of the 2m plasmid, as well as centomeric and integrative yeast shuttle vectors; vectors useful in eukaryotic cells such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or the expression control sequences; and the like.

[0129] For example in a baculovirus expression system, both non-fusion transfer vectors, such as, but not limited to pVL941 (*Bam*HI cloning site Summers, pVL1393 (*Bam*HI, *Smal*, *Xbal*, *Eco*RI, *Notl*, *Xmal*II, *Bgl*II and *Pst*I cloning sites; Invitrogen) pVL1392 (*Bg*III, *Pst*I, *Notl*, *Xmal*II, *Eco*RI, *Xbal*I, *Smal* and *Bam*HI cloning site; Summers and Invitrogen) and pBlueBacIII (*Bam*HI, *Bgl*II, *Pst*I, *Nco*I and *Hind*III cloning site, with blue/white recombinant screening, Invitrogen), and fusion transfer vectors such as, but not limited to, pAc700(*Bam*HI and *Kpn*I cloning sites, in which the *Bam*HI recognition site begins with the initiation codon; Summers), pAc701 and pAc70-2 (same as pAc700, with different reading frames), pAc360 (*Bam*HI cloning site 36 base pairs downstream of a polyhedrin initiation codon; Invitrogen (195)) and pBlueBacHisA, B, C (three different reading frames with *Bam*HI, *Bgl*II, *Pst*I, *Nco*I and *Hind*III cloning site, an N-terminal peptide for ProBond purification and blue/white recombinant screening of plaques; Invitrogen (220) can be used.

[0130] Mammalian expression vectors contemplated for use in the invention include vectors with inducible promoters, such as the dihydrofolate reductase promoters, any expression vector with a DHFR expression cassette or a DHFR/methotrexate co-amplification vector such as pED (*Pstl*, *Sall*, Sbal, Smal and *Eco*Rl cloning sites, with the vector expressing both the cloned gene and DHFR; Kaufman, 1991). Alternatively a glutamine synthetase/methionine sulfoximine co-amplification vector, such as pEE14 (*Hind*III, *Xball*, *Smal*, *Sbal*, *Eco*Rl and *Bcll* cloning sites in which the vector expresses glutamine synthetase and the cloned gene; Celltech). A vector that directs episomal expression under the control of the Epstein Barr Virus (EBV) or nuclear antigen (EBNA) can be used such as pREP4 (*Bam*HI, *Sfil*, *Xhol*, *Notl*, *Nhel*, *Hind*III, *Nhel*, *Pvu*II and *Kpnl* cloning sites, constitutive RSV-LTR promoter, hygromycin selectable marker; Invitrogen) pCEP4 (*Bam*HI, *Sfil*, *Xhol*, *Notl*, *Nhel*, *Hind*III, *Nhel*, *Pvu*II and *Kpnl* cloning sites, constitutive hCMV

immediate early gene promoter, hygromycin selectable marker; Invitrogen), pMEP4 (*Kpn*I, *Pvu*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, *Bam*HI cloning sites, inducible methallothionein IIa gene promoter, hygromycin selectable marker, Invitrogen), pREP8 (*Bam*HI, *Xho*I, *Not*I, *Hind*III, *Nhe*I and *Kpn*I cloning sites, RSV-LTR promoter, histidinol selectable marker; Invitrogen), pREP9 (*Kpn*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, *Bam*HI cloning sites, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen).

[0131] Selectable mammalian expression vectors for use in the invention include, but are not limited to, pRc/CMV (*Hind*III, *Bst*XI, *Not*I, *Sba*I and *Apa*I cloning sites, G418 selection, Invitrogen), pRc/RSV (*Hind*II, *Spe*I, *Bst*XI, *Not*I, *Xba*I cloning sites, G418 selection, Invitrogen) and the like. Vaccinia virus mammalian expression vectors (see, for example Kaufman 1991 that can be used in the present invention include, but are not limited to, pSC11 (*Sma*I cloning site, TK- and β-gal selection), pMJ601 (*SaI*I, *Sma*I, *AfI*I, *Nat*I, *Bsp*MII, *Bam*HI, *Apa*I, *Nhe*I, *Sac*II, *Kpn*I and *Hind*III cloning sites; TK- and β-gal selection), pTKgptF1S (*Eco*RI, *Pst*I, *SaI*II, *Acc*I, *Hind*II, *Sba*I, *Bam*HI and *Hpa* cloning sites, TK or XPRT selection) and the like.

[0132] Yeast expression systems that can also be used in the present include, but are not limited to, the non-fusion pYES2 vector (*Xbal*, *Sphl*, *Shol*, *Notl*, *GstXI*, *EcoRI*, *BstXI*, *BamHI*, *Sacl*, *KpnI* and *HindIII* cloning sites, Invitrogen), the fusion pYESHisA, B, C (*XbaII*, *SphI*, *Shol*, *Notl*, *BstXI*, *EcoRI*, *BamHI*, *Sacl*, *KpnI* and *HindIII* cloning sites, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), pRS vectors and the like.

[0133] Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungi, insect, nematode and plant cells an used in the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

[0134] Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61, COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

[0135] Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, (e.g., strain DH5- α), *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyce*s and *Staphylococcus*.

[0136] Further suitable cells that can be used in the present invention include yeast cells such as those of *Saccharomyces* such as *Saccharomyces cerevisiae*.

- [0137] Besides the specific isolated complexes, as described above, the present invention relates to and also encompasses SID® polynucleotides. As explained above, for each bait polypeptide, several prey polypeptides may be identified by comparing and selecting the intersection of every isolated fragment that are included in the same polypeptide. Thus the SID® polynucleotides of the present invention are represented by the shared nucleic acid sequences of SEQ ID Nos. 15 to 215 encoding the SID® polypeptides of SEQ ID Nos. 216 to 416 in columns 5 and 7 of Table III, respectively.
- [0138] The present invention is not limited to the SID® sequences as described in the above paragraph, but also includes fragments of these sequences having at least 12 consecutive nucleic acids, between 12 and 5,000 consecutive nucleic acids and between 12 and 10,000 consecutive nucleic acids and between 12 and 20,000 consecutive nucleic acids, as well as variants thereof. The fragments or variants of the SID® sequences possess at least the same affinity of binding to its protein or polypeptide counterpart, against which it has been initially selected. Moreover this variant and/or fragments of the SID® sequences alternatively can have between 95% and 99.999% sequence identity to its protein or polypeptide counterpart.
- [0139] According to the present invention the variants can be created by known mutagenesis techniques either *in vitro* or *in vivo*. Such a variant can be created such that it has altered binding characteristics with respect to the target protein and more specifically that the variant binds the target sequence with either higher or lower affinity.
- [0140] Polynucleotides that are complementary to the above sequences which include the polynucleotides of the SID®'s, their fragments, variants and those that have specific sequence identity are also included in the present invention.
- [0141] The polynucleotide encoding the SID® polypeptide, fragment or variant thereof can also be inserted into recombinant vectors which are described in detail above.
- [0142] The present invention also relates to a composition comprising the above-mentioned recombinant vectors containing the SID® polypeptides in Table III, fragments or variants thereof, as well as recombinant host cells transformed by the vectors. The recombinant host cells that can be used in the present invention were discussed in greater detail above.
- [0143] The compositions comprising the recombinant vectors can contain physiological acceptable carriers such as diluents, adjuvants, excipients and any vehicle in which this composition can be delivered therapeutically and can include, but is are not limited to sterile liquids such as water and oils.
- [0144] In yet another embodiment, the present invention relates to a method of selecting modulating compounds, as well as the modulating molecules or compounds themselves which may be used in a pharmaceutical composition. These modulating compounds may

act as a cofactor, as an inhibitor, as antibodies, as tags, as a competitive inhibitor, as an activator or alternatively have agonistic or antagonistic activity on the protein-protein interactions.

[0145] The activity of the modulating compound does not necessarily, for example, have to be 100% activation or inhibition. Indeed, even partial activation or inhibition can be achieved that is of pharmaceutical interest.

[0146] The modulating compound can be selected according to a method which comprises:

[0147] cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:

[0148] wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain;

[0149] wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;

[0150] selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.

[0151] Thus, the present invention relates to a modulating compound that inhibits the protein-protein interactions between *Shigella flexneri* polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively. The present invention also relates to a modulating compound that activates the protein-protein interactions between *Shigella flexneri* polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively.

[0152] In yet another embodiment, the present invention relates to a method of selecting a modulating compound, which modulating compound inhibits the interaction between *Shigella flexneri* polypeptide and human placenta polypeptide of columns 1 and 3 of Table II, respectively. This method comprises:

- (a) cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:
- (i) wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a first domain of an enzyme;
- (ii) wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having an enzymatic transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;

- (b) selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.
- [0153] In the two methods described above any toxic reporter gene can be utilized including those reporter genes that can be used for negative selection including the URA3 gene, the CYH1 gene, the CYH2 gene and the like.
- [0154] In yet another embodiment, the present invention provides a kit for screening a modulating compound. This kit comprises a recombinant host cell which comprises a reporter gene the expression of which is toxic for the recombinant host cell. The host cell is transformed with two vectors. The first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain; and a second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact.
- [0155] In yet another embodiment a kit is provided for screening a modulating compound by providing a recombinant host cell, as described in the paragraph above, but instead of a DNA binding domain, the first vector comprises a first hybrid polypeptide containing a first domain of a protein. The second vector comprises a second polypeptide containing a second part of a complementary domain of a protein that activates the toxic reporter gene when the first and second hybrid polypeptides interact.
- [0156] In the selection methods described above, the activating domain can be p42 Gal 4, YP16 (HSV) and the DNA-binding domain can be derived from Gal4 or Lex A. The protein or enzyme can be adenylate cyclase, guanylate cyclase, DHFR and the like.
- [0157] Examples of modulating compounds are set forth in Table III.
- [0158] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising the modulating compounds for preventing or treating bacillary dysentery in a human or animal, most preferably in a mammal.
- [0159] This pharmaceutical composition comprises a pharmaceutically acceptable amount of the modulating compound. The pharmaceutically acceptable amount can be estimated from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes or encompasses a concentration point or range having the desired effect in an *in vitro* system. This information can thus be used to accurately determine the doses in other mammals, including humans and animals.
- [0160] The therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or in experimental animals. For example, the LD50 (the dose lethal to 50% of the population) as

well as the ED50 (the dose therapeutically effective in 50% of the population) can be determined using methods known in the art. The dose ratio between toxic and therapeutic effects is the therapeutic index which can be expressed as the ratio between LD 50 and ED50 compounds that exhibit high therapeutic indexes.

- [0161] The data obtained from the cell culture and animal studies can be used in formulating a range of dosage of such compounds which lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity.
- [0162] The pharmaceutical composition can be administered via any route such as locally, orally, systemically, intravenously, intramuscularly, mucosally, using a patch and can be encapsulated in liposomes, microparticles, microcapsules, and the like. The pharmaceutical composition can be embedded in liposomes or even encapsulated.
- [0163] Any pharmaceutically acceptable carrier or adjuvant can be used in the pharmaceutical composition. The modulating compound will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" Mack Publication Co., Easton, PA, latest edition.
- [0164] The mode of administration optimum dosages and galenic forms can be determined by the criteria known in the art taken into account the seriousness of the general condition of the mammal, the tolerance of the treatment and the side effects.
- [0165] The present invention also relates to a method of treating or preventing bacillary dysentery in a human or mammal in need of such treatment. This method comprises administering to a mammal in need of such treatment a pharmaceutically effective amount of a modulating compound which binds to a targeted Shigella protein. In a preferred embodiment, the modulating compound is a polynucleotide which may be placed under the control of a regulatory sequence which is functional in the mammal or human.
- [0166] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a SID® polypeptide, a fragment or variant thereof. The SID® polypeptide, fragment or variant thereof can be used in a pharmaceutical composition provided that it is endowed with highly specific binding properties to a bait polypeptide of interest.

- [0167] The original properties of the SID® polypeptide or variants thereof interfere with the naturally occurring interaction between a first protein and a second protein within the cells of the organism. Thus, the SID® polypeptide binds specifically to either the first polypeptide or the second polypeptide.
- [0168] Therefore, the SID® polypeptides of the present invention or variants thereof interfere with protein-protein interactions between *Shigella* or *Escherichia* polypeptides or between a mammal polypeptide.
- [0169] Thus, the present invention relates to a pharmaceutical composition comprising a pharmaceutically acceptable amount of a SID® polypeptide or variant thereof, provided that the variant has the above-mentioned two characteristics; i.e., that it is endowed with highly specific binding properties to a bait polypeptide of interest and is devoid of biological activity of the naturally occurring protein.
- [0170] In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a pharmaceutically effective amount of a polynucleotide encoding a SID® polypeptide or a variant thereof wherein the polynucleotide is placed under the control of an appropriate regulatory sequence. Appropriate regulatory sequences that are used are polynucleotide sequences derived from promoter elements and the like.
- [0171] Polynucleotides that can be used in the pharmaceutical composition of the present invention include the nucleotide sequences of SID®s of SEQ ID Nos. 15 to 215.
- [0172] Besides the SID® polypeptides and polynucleotides, the pharmaceutical composition of the present invention can also include a recombinant expression vector comprising the polynucleotide encoding the SID® polypeptide, fragment or variant thereof.
- [0173] The above described pharmaceutical compositions can be administered by any route such as orally, systemically, intravenously, intramuscularly, intradermally, mucosally, encapsulated, using a patch and the like. Any pharmaceutically acceptable carrier or adjuvant can be used in this pharmaceutical composition.
- [0174] The SID® polypeptides as active ingredients will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" supra.
- [0175] The amount of pharmaceutically acceptable SID® polypeptides can be determined as described above for the modulating compounds using cell culture and animal models.
- [0176] Such compounds can be used in a pharmaceutical composition to treat or prevent bacillary dysentery.
- [0177] Thus, the present invention also relates to a method of preventing or treating bacillary dysentery in a mammal said method comprising the steps of administering to a

mammal in need of such treatment a pharmaceutically effective amount of a recombinant expression vector comprising a polynucleotide encoding a SID® polypeptide which binds to a either to a *Shigella flexneri* protein or to a human placenta protein involved in a protein-protein interaction between a *Shigella flexneri* protein and an human placenta protein. More specifically, the present invention relates to a method of preventing or treating bacillary dysentery in a mammal said method comprising the steps of administering to a mammal in need of such treatment a pharmaceutically effective amount of:

- (1) a SID® polypeptide of SEQ ID Nos. 216 to 416 or a variant thereof which binds to a targeted *Shigella flexneri* protein or human placenta protein; or
- (2) a SID® polynucleotide encoding a SID® polypeptide of SEQ ID Nos. 15 to 215 or a variant or a fragment thereof wherein said polynucleotide is placed under the control of a regulatory sequence which is functional in said mammal; or
- (3) a recombinant expression vector comprising a polynucleotide encoding a SID® polypeptide which binds either to a *Shigella flexneri* protein or to a human placenta protein involved in a protein-protein interaction between a *Shigella flexneri* protein and an human placenta protein.
- [0178] In another embodiment the present invention nucleic acids comprising a sequence of SEQ ID Nos. 15 to 215 which encodes the protein of sequence SEQ ID Nos. 216 to 416 and/or functional derivatives thereof are administered to modulate complex (from Table II) function by way of gene therapy. Any of the methodologies relating to gene therapy available within the art may be used in the practice of the present invention such as those described by Goldspiel et al *Clin. Pharm.* 12 pgs. 488-505 (1993).
- [0179] Delivery of the therapeutic nucleic acid into a patient may be direct *in vivo* gene therapy (i.e., the patient is directly exposed to the nucleic acid or nucleic acid-containing vector) or indirect *ex vivo* gene therapy (i.e., cells are first transformed with the nucleic acid in vitro and then transplanted into the patient).
- [0180] For example for *in vivo* gene therapy, an expression vector containing the nucleic acid is administered in such a manner that it becomes intracellular; i.e., by infection using a defective or attenuated retroviral or other viral vectors as described, for example in U.S. Patent 4,980,286 or by Robbins et al, Pharmacol. *Ther.*, 80 No. 1 pgs. 35-47 (1998).
- [0181] The various retroviral vectors that are known in the art are such as those described in Miller et al, *Meth. Enzymol.* 217 pgs. 581-599 (1993) which have been modified to delete those retroviral sequences which are not required for packaging of the viral genome and subsequent integration into host cell DNA. Also adenoviral vectors can be used which are advantageous due to their ability to infect non-dividing cells and such high-capacity adenoviral vectors are described in Kochanek, *Human Gene Therapy*, 10, pgs. 2451-2459 (1999). Chimeric viral vectors that can be used are those described by Reynolds

et al, *Molecular Medecine Today*, pgs. 25 –31 (1999). Hybrid vectors can also be used and are described by Jacoby et al, *Gene Therapy*, **4**, pgs. 1282-1283 (1997).

[0182] Direct injection of naked DNA or through the use of microparticle bombardment (e.g., Gene Gun®; Biolistic, Dupont). or by coating it with lipids can also be used in gene therapy. Cell-surface receptors/transfecting agents or through encapsulation in liposomes, microparticles or microcapsules or by administering the nucleic acid in linkage to a peptide which is known to enter the nucleus or by administering it in linkage to a ligand predisposed to receptor-mediated endocytosis (See, Wu & Wu, J. Biol. Chem., 262 pgs. 4429-4432 (1987)) can be used to target cell types which specifically express the receptors of interest.

[0183] In another embodiment a nucleic acid ligand compound may be produced in which the ligand comprises a fusogenic viral peptide designed so as to disrupt endosomes, thus allowing the nucleic acid to avoid subsequent lysosomal degradation. The nucleic acid may be targeted *in vivo* for cell specific endocytosis and expression by targeting a specific receptor such as that described in WO92/06180, WO93/14188 and WO 93/20221. Alternatively the nucleic acid may be introduced intracellularly and incorporated within the host cell genome for expression by homologous recombination. See, Zijlstra et al, *Nature*, 342, pgs. 435-428 (1989).

[0184] In ex vivo gene a gene is transferred into cells in vitro using tissue culture and the cells are delivered to the patient by various methods such as injecting subcutaneously, application of the cells into a skin graft and the intravenous injection of recombinant blood cells such as hematopoietic stem or progenitor cells.

[0185] Cells into which a nucleic acid can be introduced for the purposes of gene therapy include, for example, epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes and blood cells. The blood cells that can be used include, for example, T-lymphocytes, B-lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryotcytes, granulocytes, hematopoietic cells or progenitor cells and the like.

[0186] In yet another embodiment the present invention relates to protein chips or protein microarrays. It is well known in the art that microarrays can contain more than 10,000 spots of a protein that can be robotically deposited on a surface of a glass slide or nylon filter. The proteins attach covalently to the slide surface, yet retain their ability to interact with other proteins or small molecules in solution. In some instances the protein samples can be made to adhere to glass slides by coating the slides with an aldehydecontaining reagent that attaches to primary amines. A process for creating microarrays is described, for example by MacBeath and Schreiber in *Science*, Volume 289, Number 5485, pgs, 1760-1763 (2000) or Service, *Science*, Vol, 289, Number 5485 pg. 1673 (2000). An

apparatus for controlling, dispensing and measuring small quantities of fluid is described, for example, in U.S. Patent No. 6,112,605.

[0187] The present invention also provides a record of protein-protein interactions, PIM®'s, SID®'s and any data encompassed in the following Tables. It will be appreciated that this record can be provided in paper or electronic or digital form.

[0188] In order to fully illustrate the present invention and advantages thereof, the following specific examples are given, it being understood that the same are intended only as illustrative and in no way limitative.

EXAMPLES

EXAMPLE 1: Preparation of a collection of random-primed cDNA fragments

1.A. Collection preparation and transformation in Escherichia coli

1.A.1. Random-primed cDNA fragment preparation

[0189] For the human placenta mRNA sample, random-primed cDNA was prepared from 5 μ g of polyA+ mRNA using a TimeSaver cDNA Synthesis Kit (Amersham Pharmacia Biotech) and with 5 μ g of random N9-mers according to the manufacturer's instructions. Following phenolic extraction, the cDNA was precipitated and resuspended in water. The resuspended cDNA was phosphorylated by incubating in the presence of T4 DNA Kinase (Biolabs) and ATP for 30 minutes at 37°C. The resulting phosphorylated cDNA was then purified over a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.

1.A.2. Ligation of linkers to blunt-ended cDNA

Oligonucleotide HGX931 (5' end phosphorylated) 1 μ g/ μ l and HGX932 1 μ g/ μ l.

Sequence of the oligo HGX931: 5'-GGGCCACGAA-3' (SEQ ID NO. 417)

Sequence of the oligo HGX932 : 5'-TTCGTGGCCCCTG-3' (SEQ ID NO. 418)

[0190] Linkers were preincubated (5 minutes at 95°C, 10 minutes at 68°C, 15 minutes at 42°C) then cooled down at room temperature and ligated with cDNA fragments at 16°C overnight.

[0191] Linkers were removed on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.

1.A.3. Vector preparation

[0192] Plasmid pP6 (see Figure 10) was prepared by replacing the *SpellXhol* fragment of pGAD3S2X with the double-stranded oligonucleotide:

- [0193] The pP6 vector was successively digested with *Sfi*1 and *Bam*HI restriction enzymes (Biolabs) for 1 hour at 37°C, extracted, precipitated and resuspended in water. Digested plasmid vector backbones were purified on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer's protocol.
- 1.A.4. Ligation between vector and insert of cDNA
- [0194] The prepared vector was ligated overnight at 15°C with the blunt-ended cDNA described in section 2 using T4 DNA ligase (Biolabs). The DNA was then precipitated and resuspended in water.
- 1.A.5. Library transformation in Escherichia coli
- [0195] The DNA from section 1.A.4 was transformed into Electromax DH10B electrocompetent cells (Gibco BRL) with a Cell Porator apparatus (Gibco BRL). 1 ml SOC medium was added and the transformed cells were incubated at 37°C for 1 hour. 9 mls of SOC medium per tube was added and the cells were plated on LB+ampicillin medium. The colonies were scraped with liquid LB medium, aliquoted and frozen at -80°C.
- [0196] The obtained collection of recombinant cell clones is named HGXBPLARP1.
- 1.B. Collection transformation in Saccharomyces cerevisiae
- [0197] The Saccharomyces cerevisiae strain (Y187 (MAT α Gal4 Δ Gal80 Δ ade2-101, his3, leu2-3, -112, trp1-901, ura3-52 URA3::UASGAL1-LacZ Met)) was transformed with the cDNA library.
- [0198] The plasmid DNA contained in E. coli were extracted (Qiagen) from aliquoted E. coli frozen cells (1.A.5.). Saccharomyces cerevisiae yeast Y187 in YPGlu were grown.
- [0199] Yeast transformation was performed according to standard protocol (Giest et al. Yeast, 11, 355-360, 1995) using yeast carrier DNA (Clontech). This experiment leads to 10^4 to 5×10^4 cells/µg DNA. 2×10^4 cells were spread on DO-Leu medium per plate. The cells were aliquoted into vials containing 1 ml of cells and frozen at -80°C.
- [0200] The obtained collection of recombinant cell clones is named HGXYPLARP1 (placenta).
- 1.C. Construction of bait plasmids
- [0201] For fusions of the bait protein (listed in Table II) to the DNA-binding domain of the GAL4 protein of *S. cerevisiae*, bait fragments were cloned into plasmid pB6. For fusions of the bait protein to the DNA-binding domain of the LexA protein of *E. coli*, bait fragments were cloned into plasmid pB20.
- [0202] Plasmid pB6 (see Figure 3) was prepared by replacing the Nco1/Sal1 polylinker fragment of pAS $\Delta\Delta$ with the double-stranded DNA fragment:

3'

[0203] Plasmid pB20 (see Figure 6) was prepared by replacing the *Eco*RI*PstI* polylinker fragment of pLex10 with the double-stranded DNA fragment:

5'

3'

[0204] The amplification of the bait ORF was obtained by PCR using the Pfu proof-reading *Taq* polymerase (Stratagene), 10 pmol of each specific amplification primer and 200 ng of plasmid DNA as template.

[0205] The PCR program was set up as follows:

[0206] The amplification was checked by agarose gel electrophoresis.

[0207] The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol.

[0208] Purified PCR fragments were digested with adequate restriction enzymes. The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol.

[0209] The digested PCR fragments were ligated into an adequately digested and dephosphorylated bait vector (pB6 or pB20) according to standard protocol (Sambrook *et al.*) and were transformed into competent bacterial cells. The cells were grown, the DNA extracted and the plasmid was sequenced.

Example 2: Screening the collection with the two-hybrid in yeast system

2.A. The mating protocol

[0210] The mating two-hybrid in yeast system (as described by Legrain et al., *Nature Genetics*, vol. 16, 277-282 (1997), *Toward a functional analysis of the yeast genome through*

exhaustive two-hybrid screens) was used for its advantages but one could also screen the cDNA collection in classical two-hybrid system as described in Fields et al. or in a yeast reverse two-hybrid system.

[0211] The mating procedure allows a direct selection on selective plates because the two fusion proteins are already produced in the parental cells. No replica plating is required.

[0212] This protocol was written for the use of the library transformed into the Y187 strain.

[0213] For bait proteins fused to the DNA-binding domain of GAL4, bait-encoding plasmids were first transformed into *S. cerevisiae* (CG1945 strain (MATa Gal4-542 Gal180-538 ade2-101 his3∆200, leu2-3,112, trp1-901, ura3-52, lys2-801, URA3::GAL4 17mers (X3)-CyC1TATA-LacZ, LYS2::GAL1UAS-GAL1TATA-HIS3 CYH^R)) according to step 1.B. and spread on DO-Trp medium.

[0214] For bait proteins fused to the DNA-binding domain of LexA, bait-encoding plasmids were first transformed into *S. cerevisiae* (L40\(\Delta\)gal4 strain (MATa ade2, trp1-901, leu2 3,112, lys2-801, his3\(\Delta\)200, LYS2::(lexAop)₄-HIS3, ura3-52::URA3 (lexAop)₈-LacZ, GAL4::Kan^R)) according to step 1.B. and spread on DO-Trp medium.

Day 1, morning: preculture

[0215] The cells carrying the bait plasmid obtained at step 1.C. were precultured in 20 ml DO-Trp medium and grown at 30°C with vigorous agitation.

Day 1, late afternoon: culture

[0216] The OD_{600nm} of the DO-Trp pre-culture of cells carrying the bait plasmid pre-culture was measured. The OD_{600nm} must lie between 0.1 and 0.5 in order to correspond to a linear measurement.50 ml DO-Trp at OD_{600nm} 0.006/ml was inoculated and grown overnight at 30°C with vigorous agitation.

Day 2: mating

medium and plates

1 YPGlu 15cm plate

50 ml tube with 13 ml DO-Leu-Trp-His

100 ml flask with 5 ml of YPGlu

8 DO-Leu-Trp-His plates

2 DO-Leu plates

2 DO-Trp plates

2 DO-Leu-Trp plates

[0217] The OD_{600nm} of the DO-Trp culture was measured. It should be around 1.

[0218] For the mating, twice as many bait cells as library cells were used. To get a good mating efficiency, one must collect the cells at 10⁸ cells per cm².

[0219] The amount of bait culture (in ml) that makes up 50 OD_{600nm} units for the mating with the prey library was estimated.

[0220] A vial containing the HGXYCDNA1 library was thawed slowly on ice. 1.0ml of the vial was added to 5 ml YPGlu. Those cells were recovered at 30°C, under gentle agitation for 10 minutes.

Mating

- [0221] The 50 OD600nm units of bait culture was placed into a 50 ml falcon tube.
- [0222] The HGXYCDNA1 library culture was added to the bait culture, then centrifuged, the supernatant discarded and resuspended in 1.6ml YPGlu medium.
- [0223] The cells were distributed onto two 15cm YPGlu plates with glass beads. The cells were spread by shaking the plates. The plate cells-up at 30°C for 4h30min were incubated.

Collection of mated cells

[0224] The plates were washed and rinsed with 6ml and 7ml respectively of DO-Leu-Trp-His. Two parallel serial ten-fold dilutions were performed in 500µl DO-Leu-Trp-His up to 1/10,000. 50µl of each 1/10000 dilution was spread onto DO-Leu and DO-trp plates and 50µl of each 1/1000 dilution onto DO-Leu-Trp plates. 22.4ml of collected cells were spread in 400µl aliquots on DO-Leu-Trp-His+Tet plates.

Day 4

- [0225] Clones that were able to grow on DO-Leu-Trp-His+Tetracyclin were then selected. This medium allows one to isolate diploid clones presenting an interaction.
- [0226] The His+ colonies were counted on control plates.
- [0227] The number of His+ cell clones will define which protocol is to be processed:
- [0228] Upon 60.10⁶ Trp+Leu+ colonies:
- if the number His+ cell clones <285 : then use the process luminometry protocol on all colonies
- if the number of His+ cell clones > 285 and <5000: then process via overlay and then luminometry protocols on blue colonies (2.B and 2.C).
- if number of His+ cell clones >5000 : repeat screen using DO-Leu-Trp-His+Tetracyclin plates containing 3-aminotriazol.
- 2.B. The X-Gal overlay assay
- [0229] The X-Gal overlay assay was performed directly on the selective medium plates after scoring the number of His⁺ colonies.

Materials

- [0230] A waterbath was set up. The water temperature should be 50°C.
- 0.5 M Na₂HPO₄ pH 7.5.
- 1.2% Bacto-agar.

2% X-Gal in DMF.

Overlay mixture: 0.25 M Na₂HPO₄ pH7.5, 0.5% agar, 0.1% SDS, 7% DMF (LABOSI), 0.04% X-Gal (ICN). For each plate, 10 ml overlay mixture are needed.

DO-Leu-Trp-His plates.

Sterile toothpicks.

Experiment

[0231] The temperature of the overlay mix should be between 45°C and 50°C. The overlay-mix was poured over the plates in portions of 10 ml. When the top layer was settled, they were collected. The plates were incubated overlay-up at 30°C and the time was noted. Blue colonies were checked for regularly. If no blue colony appeared, overnight incubation was performed. Using a pen the number of positives was marked. The positives colonies were streaked on fresh DO-Leu-Trp-His plates with a sterile toothpick.

2.C. The luminometry assay

[0232] His+ colonies were grown overnight at 30°C in microtiter plates containing DO-Leu-Trp-His+Tetracyclin medium with shaking. The day after, the overnight culture was diluted 15 times into a new microtiter plate containing the same medium and was incubated for 5 hours at 30°C with shaking. The samples were diluted 5 times and read OD_{600nm} . The samples were diluted again to obtain between 10,000 and 75,000 yeast cells/well in 100 μ l final volume.

[0233] Per well, 76 μ l of One Step Yeast Lysis Buffer (Tropix) was added, 20 μ l SapphireII Enhancer (Tropix), 4 μ l Galacton Star (Tropix) and incubated 40 minutes at 30°C. The β -Gal read-out (L) was measured using a Luminometer (Trilux, Wallach). The value of (OD_{600nm} x L) was calculated and interacting preys having the highest values were selected.

[0234] At this step of the protocol, diploid cell clones presenting interaction were isolated. The next step was now to identify polypeptides involved in the selected interactions.

Example 3: Identification of positive clones

3.A. PCR on yeast colonies

Introduction

[0235] PCR amplification of fragments of plasmid DNA directly on yeast colonies is a quick and efficient procedure to identify sequences cloned into this plasmid. It is directly derived from

[0236] a published protocol (Wang H. et al., *Analytical Biochemistry*, **237**, 145-146, (1996)). However, it is not a standardized protocol and it varies from strain to strain and it is dependent of experimental conditions (number of cells, *Taq* polymerase source, etc). This protocol should be optimized to specific local conditions.

Materials

[0237] For 1 well, PCR mix composition was:

32.5 µl water,

5 μl 10X PCR buffer (Pharmacia),

1 μl dNTP 10 mM,

0.5 μl Taq polymerase (5u/μl) (Pharmacia),

0.5 μl oligonucleotide ABS1 10 pmole/μl: 5'-GCGTTTGGAATCACTACAGG-3',(SEQ ID NO. 424)

0.5 μl oligonucleotide ABS2 10 pmole/μl: 5'-CACGATGCACGTTGAAGTG-3'.(SEQ ID NO. 425)

1 N NaOH.

Experiment

[0238] The positive colonies were grown overnight at 30°C on a 96 well cell culture cluster (Costar), containing 150 μ l DO-Leu-Trp-His+Tetracyclin with shaking. The culture was resuspended and 100 μ l was transferred immediately on a Thermowell 96 (Costar) and centrifuged for 5 minutes at 4,000 rpm at room temperature. The supernatant was removed. 5 μ l NaOH was added to each well and shaken for 1 minute.

[0239] The Thermowell was placed in the thermocycler (GeneAmp 9700, Perkin Elmer) for 5 minutes at 99.9°C and then 10 minutes at 4°C. In each well, the PCR mix was added and shaken well.

[0240] The PCR program was set up as followed:

94°C	3 minutes	
94°C	30 seconds	
53°C	1 minute 30 seconds	x 35 cycles
72°C	3 minutes	
72°C	5 minutes	
15°C	ω	

[0241] The quality, the quantity and the length of the PCR fragment was checked on an agarose gel. The length of the cloned fragment was the estimated length of the PCR fragment minus 300 base pairs that corresponded to the amplified flanking plasmid sequences.

[0242] 3.B. Plasmids rescue from yeast by electroporation Introduction

[0243] The previous protocol of PCR on yeast cell may not be successful, in such a case, plasmids from yeast by electroporation can be rescued. This experiment allows the recovery of prey plasmids from yeast cells by transformation of *E. coli* with a yeast cellular extract. The prey plasmid can then be amplified and the cloned fragment can be sequenced. Materials

[0244] Plasmid rescue

Glass beads 425-600 μm (Sigma)Phenol/chloroform (1/1) premixed with isoamyl alcohol (Amresco)

Extraction buffer: 2% Triton X100, 1% SDS, 100 mM NaCl, 10 mM TrisHCl pH 8.0, 1 mM EDTA pH 8.0.

Mix ethanol/NH $_4$ Ac : 6 volumes ethanol with 7.5 M NH $_4$ Acetate, 70% Ethanol and yeast cells in patches on plates.

Electroporation

SOC medium

M9 medium

Selective plates: M9-Leu+Ampicillin

2 mm electroporation cuvettes (Eurogentech)

Experiment

Plasmid rescue

[0245] The cell patch on DO-Leu-Trp-His was prepared with the cell culture of section 2.C. The cell of each patch was scraped into an Eppendorf tube, 300 μ l of glass beads was added in each tube, then, 200 μ l extraction buffer and 200 μ l phenol:chloroform:isoamyl alcohol (25:24:1) was added.

[0246] The tubes were centrifuged for 10 minutes at 15,000 rpm.

[0247] 180 μ l supernatant was transferred to a sterile Eppendorf tube and 500 μ l each of ethanol/NH₄Ac was added and the tubes were vortexed. The tubes were centrifuged for 15 minutes at 15,000 rpm at 4°C. The pellet was washed with 200 μ l 70% ethanol and the ethanol was removed and the pellet was dried. The pellet was resuspended in 10 μ l water. Extracts were stored at -20°C.

Electroporation

Materials:

[0248] Electrocompetent MC1066 cells prepared according to standard protocols (Sambrook et al. *supra*).

1 μ l of yeast plasmid DNA-extract was added to a pre-chilled Eppendorf tube, and kept on ice.

1 μ l plasmid yeast DNA-extract sample was mixed and 20 μ l electrocompetent cells was added and transferred in a cold electroporation cuvette. Set the Biorad electroporator on 200 ohms resistance, 25 μ F capacity; 2.5 kV. Place the cuvette in the cuvette holder and electroporate.

1 ml of SOC was added into the cuvette and the cell-mix was transferred into a sterile Eppendorf tube. The cells were recovered for 30 minutes at 37°C, then spun down for

1 minute at 4,000 x g and the supernatant was poured off. About 100 μ l medium was kept and used to resuspend the cells and spread them on selective plates (e.g., M9-Leu plates). The plates were then incubated for 36 hours at 37°C.

[0249] One colony was grown and the plasmids were extracted. Check for the presence and size of the insert through enzymatic digestion and agarose gel electrophoresis. The insert was then sequenced.

Example 4: Protein-protein interaction

[0250] For each bait, the previous protocol leads to the identification of prey polynucleotide sequences. Using a suitable software program (e.g., Blastwun, available on the Internet site of the University of Washington: http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.html) the identity of the mRNA transcript that is encoded by the prey fragment may be determined and whether the fusion protein encoded is in the same open reading frame of translation as the predicted protein or not.

[0251] Alternatively, prey nucleotide sequences can be compared with one another and those which share identity over a significant region (60nt) can be grouped together to form a contiguous sequence (Contig) whose identity can be ascertained in the same manner as for individual prey fragments described above.

Example 5: Identification of SID®

[0252] By comparing and selecting the intersection of all isolated fragments that are included in the same polypeptide, one can define the Selected Interacting Domain (SID®) as illustrated in Figure 15. The SID® is illustrated in Table III.

Example 6: Identification of PIM®

[0253] The PIM® is then constructed using methods known in the art as exemplified in Figure 16.

Example 7: Making of polyclonal and monoclonal antibodies

[0254] The protein-protein complex of columns 1 and 3 of Table II was injected into mice and polyclonal and monoclonal antibodies were made following the procedure set forth in Sambrook et al. (*supra*).

[0255] More specifically, mice are immunized with an immunogen comprising Table II complexes conjugated to keyhole limpet hemocyanin using glutaraldehyde or EDC as is well known in the art. The complexes can also be stabilized by crosslinking as described in WO 00/37483. The immunogen is then mixed with an adjuvant. Each mouse receives four injections of 10 ug to 100 ug of immunogen, and after the fourth injection, blood samples are taken from the mice to determine if the serum contains antibodies to the immunogen. Serum titer is determined by ELISA or RIA. Mice with sera indicating the presence of antibody to the immunogen are selected for hybridoma production.

[0256] Spleens are removed from immune mice and single-cell suspension is prepared (Harlow et al 1988). Cell fusions are performed essentially as described by Kohler et al (1976). Briefly, P365.3 myeloma cells (ATTC Rockville, Md) or NS-1 myeloma cells are fused with spleen cells using polyethylene glycol as described by Harlow et al (1989). Cells are plated at a density of 2 x 10⁵ cells/well in 96-well tissue culture plates. Individual wells are examined for growth and the supernatants of wells with growth are tested for the presence of the complex-specific antibodies by ELISA or RIA using one of the proteins set forth in Table II as a target protein. Cells in positive wells are expanded and subcloned to establish and confirm monoclonality.

[0257] Clones with the desired specificities are expanded and grown as ascites in mice or in a hollow fiber system to produce sufficient quantities of antibodies for characterization and assay development. Antibodies are tested for binding to one of the proteins in Table II, to determine which are specific for the Table II complexes as opposed to those that bind to the individual proteins. More specifically, antibodies are tested for binding to bait polypeptide of column 1 of Table II alone or to prey polypeptide of column 3 of Table II alone, to determine which are specific for the protein-protein complex of columns 1 and 3 of Table II as opposed to those that bind to the individual proteins.

[0258] Monoclonal antibodies against each of the complexes set forth in columns 1 and 3 of Table II are prepared in a similar manner by mixing specified proteins together, immunizing an animal, fusing spleen cells with myeloma cells and isolating clones which produce antibodies specific for he protein complex, but not for individual proteins.

Example 8: Modulating compounds/PIM screening

[0259] Each specific protein-protein complex of columns 1 and 3 of Table II may be used to screen for modulating compounds.

[0260] One appropriate construction for this modulating compound screening may be:

- bait polynucleotide inserted in pB6 or pB20;- prey polynucleotide inserted in pP6;
- transformation of these two vectors in a permeable yeast cell;
- growth of the transformed yeast cell on medium containing compound to be tested;
- and observation of the growth of the yeast cells.
- [0261] The following results obtained from these Examples, as well as the teachings in the specification are set forth in the Tables below.
- [0262] While the invention has been described in terms of the various preferred embodiments, the skilled artisan will appreciate that various modifications, substitutions, omissions and changes may be made without departing from the scope thereof. Accordingly, it is intended that the present invention be limited by the scope of the following claims, including equivalents thereof.

[0263] All patent and non-patent publications cited in this specification, including the websites set forth onpages 8, 13 and 33, are indicative of the level of skill of those skilled in the art to which this invention pertains. All these publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated herein by reference.

	MNLDGVRPYCRIVNKKNESISDIAFAHIIKRVKNS SCTHPKAALVFLGEKGFCDSNDVLSIMGQQIPR VFKNKMLYDYVFKNEKSKNDFLKMAESWLPQS EPIVINNDDDALNAAAYFSVKKAKIKTVNDTDFKE YNKVYILGHGSPGSHQLGLGSELIDVQTIISRMK DCGILNVKDIRFTSCGSADKVAPKNFNNAPAESL SCILNSLPFFKEKESLLEQIKKHLENDESLSDGLK ISGYHGYGVHYGQELFPYSHYRSTSIPADPEHT VKRSSQKKTFIINKELD*YKIFNL*	MSINNYGLHPANNKNMHLIIGSNTANENKGMKN NIINYTNTAISHAINEEKSGGGYSGVSFRKLAKIQ NISIPTKNNKEYNRHNLFSLIWHGNADAARKYSE
5: Amino- acid ID No.	ω	<u>თ</u>
4: Nucleic Positions	[1-888]	[1-711]
3: Nucleic acid sequence	TIGAATITIAGATGGTGTTAGACCATACTGTAGAA TAGTCAATAAAAAGAGCATATCAGATAT TCATCATGTACACATAAAAAGGGTAAAAAAAA TCATCATGTACTCACCCAAAGCGCATTGGTTT TTTAGGAGAGAAAGGTTTTTGTGATAGCAATGA TGTTCTATCTATTATGGACACAAATACAAGA GTATTTAAGAAAAGGTTTTTGTGATTATGTTTT TAAAAATGAAAAAGGTTTTTCTAAAAA TGGCTGAATCATGGCTACCACAGAGTGATTT TAGTAATAAATAATGTGATTATGATTTTCTAAAA TGGCTGAATCATGGCTACCACAGAGTGAAAA TGCTGATTATTTTCTGTAAAAAAAAGCGAAAATA AAAACGGTTATTTTCTGTAAAAAAAAAGGCAAAATA AAAACGATAAATGTTCTGGAAAAAAAAGGAAATTA TGTGTACTTAAATATTCTTGGAAAAAAAAGGAAAAAAAAA	TATAG ATGTCAATAAATAACTATGGATTACATCCAGCAA ACAACAAAATATGCACCTAATAATAGGCAGCAA TACTGCTAATGAAAATAAAAGGAATGAAAAATAAT
sequences 2: Nucleic acid ID No.	T-	2
1: Bait name 2: Nucleacid acid No.	Shigella ospB	Shigella ospD1

SLLAAEIPKEEKLEVLAARNNAGESALFIALQEGH SAAIQAYGDFIKTFDLSPKETIKLLDVRDNEGLPG LFLAAGKGNIEAMMAYINICHHSGIKLTEIADRLN NNEQDMFNIISDKIQELF*VC*IAAKNCT*	10 MNISETLNSANTQCNIDSMDNRLHTLFPKVTSVR NAAQQTMPDEKNLKDSANIIKDFFRKTIAAQSYS RMFSQGSNFKSLNIAIDAPSDAKASFKAIEHLDR LSKHYISEIREKLHPLSAEELNLLSLIINSDLIFRHQ SNSDLSDKILNIKSFNKIQSEGICTKRNTYADDIK KIANHDFVFFGVEISNHQKKHPLNTKHHTVDFGA NAYIIDHDSPYGYMTLTDHFDNAIPPVFYHEHQS FLDKFSEVNKEVSRYVHGSKGIIDVPIFNTKDMK LGLGLYLIDFIRKSEDQSFKEFCYGKNLAPVDLD RIINFVFQPEYHIPRMVSTENFKKVKIREISLEEAV TASNYEEINKQVTNKKIALQALFLSITNQKEDVAL YILSNYEEINKQVTNKKIALQALFLSITNQKEDVAL YILSNYEEITRQDVISIKHELYDIEYLLSAHNSSCKV LEYFINKGLVDVNTKFKKTNSGDCMLDNAIKYEN AEMIKLLLKYGATSDNKYI*SKLNIV*
	[1-1434] 1
	7
ATCATTAACGTGACAAATACCGCTATATCCCACG CCATCAATGAGAAAATCAGGGGGGGGGTATA GTGGTTTTCTTTCAGGAAATTGGCCAAAATACA GAACATATCCATTCCGACAAGATAATTAGG GAACATACCATTCCGACAAGAATAATAGGA GTATAACCGCCATAATTTGTTTCATTGATTTGG CATGGAAATGCCGATGCAGCGCGTAAATACAGT GAAAAACTGGTGCAGCCGAAATACCAAAGGA GAAAACTTGTTGTTCATAGCTCTTCAT GCTGGGGAATCTGCTTGTTCATAGCTCTTCAA GAAAACTTTTGTTGATTTATCAGGAAATAAT GCTGGGGAATCTGCTTGTTCATAGGAAAGA AACGATTAAAACTTTTGGATGTAAGAGAAAGA AACGATTAAAACTTTTGGGATGTAAGAGAAACGAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAA	ATGAATATACAGAAACACTGAACTCAGCAAATA CCCAATGCAATATAGATTCTATGGATAACAGATT ACATGCAATATAGATTCTATGGATAACAGATT ACATGCAATATAGATTCTATGGACACAGATGGAATATATAAAAAAAA
	က
	dso
	Shigella ospC1

	MNITTLTNSISTSSFSPNNTNGSSTETVNSDIKTT TSSHPVSSLTMLNDTLHNIRTTNQALKKELSQKT LTKTSLEEIALHSSQISMDVNKSAQLLDILSRNEY PINKDARELLHSAPKEAELDGDQMISHRELWAKI ANSINDINEQYLKYYEHAVSSYTQMYQDFSAVLS SLAGWISPGGNDGNSVKLQVNSLKKALEELKEK YKDKPLYPANNTVSQEQANKWLTELGGTIGKVS QKNGGYVVSINMTPIDNMLKSLDNLGGNGEVVL
	1-
	[1-1005]
TGITITITGGCGTTGAAATCTCTAACCATCAGAA AAAACACCCCCTGAATACAAAACATCACACTGTT GAAACCACCCCTGAATACAAAACATTGATCATG ACTCTCCATATGGATATTGACATTAACCGATC CTTTGATAATGCTATTCCACCTGTTTTTTACCAT GAGCACCAATCATTTTTAGATAAATTTTACAAGG TTAATAAAGAAGTTAGTCGATACGTACATACT AAAGGAATTATAGAAAAATTTTCAATACT AAAGGAATTATAGAAAAATTTTCAATACT AAAGGAATTATAGAAAAAATTTACAATACT AAAGGATTTTGCATAGGAAAAAATCTTGCCC TGTGGATTTGCATAGAAAAAATTTTTTTTTCAAAAAAAAA	ATGAATATAACAACTCTGACTAATAGTATTTCCA CCTCATCCATCCAACCACACGGTTC ATCAACCGAAACAGTTAATTCTGATATAAAAAACA ACGACCAGTCTCATCCTGTAAGTTCCCTTACTA ACGACCAGTTCATCTCATATTCCATACTACTA TGCTCAACGACCCTTCATATTCACAAAACAACAACAAACA
	4
	Shigella ipaD

	MLPINNNFSLPGNSFTN IISGITTSAWDEN EKQALPGEERDEAVSRLKECLINNSDELRLDRL NLSSLPDNLPAQITLLNVSYNQLTNLPELPVTLKK LYSASNKLSELPVLPPALESLQVQHNELENLPAL PDSLLTMNISYNEIVSLPSLPQALKNLRATRNFLT ELPAFSEGNNPVVREYFFDRNQISHIPESILNLR NECSIHISDNPLSSHALQALQRLTSSPDYHGPRI YFSMSDGQQNTLHRPLADAVTAWFPENKQSDV SQIWHAFEHEEHANTFSAFLDRLSDTVSARNTS GFREQVAAWLEKLSASAELRQQSFAVAADATES CEDR
	6
	[1-1022]
TCTCAATTGTCATTGATTGCGTTCGATGCTACAA AATCAGCTGCAGAGACATTGTTCGGCAAGGCC TGGCAGCCCTATCATCAAGCATTACTGGAGGCG TCACACAAGTAGGTATACGGGTATCGGTGCCA AAAAAACGCATTCAGGGATTAGCGGTGCCAAAAG GAGCCTTAAGAAAGAAGACCTTGCCACTGCTCAAT CTCTTGAAAAAGAAGACCTTGCCACTGCTCAAT CTCTTGAAAAAGAAGACTTGCAGGTTCTAAATTAGG GTTAAATAAACAAATAGATACAAATATCACCTCA CCACAAACTAACTCTTAGCACAAATTTTAGGTA AAAATAAACTGGCGCCAGATAATATCCCTGTC AAAATAAACTGGCGCCAGATAATATCCCCTGTC AAAATAAACTGGCGCCAAAATTGATCCCTGTC AAAATAACTGGCGCTAAAATTGATTCCCCGAT ATTTCTTTGCAGGATAAAATTGATCCCAGGAAA GAAATAAACTGGCCGTGCCAATAGGAAGAAGAA CATCAGCCGTTGCTGGTAATATATCCACATCAG GAAACTAATCGGTCAGGCAGCAAGAAGAA CCCAAGCGAAGCATCCCAAGTATTAATAAAAAAAGAAGAT CCCAAGCGACAAATCAATTAATAAAAAAAATTTT GAAATAAATTGACAATTAATAAAAAAAATTTT CCCAAGCGACAAATCAAAT	ATGTTACCGATAAATAACACTTTTCATTGCCCC AAAATTCTTTTATAACACTATTTCCGGTACATAT GCTGATTACTTTTCAGCATGGGATAAATGGGAA AAACAAGCGCTCCCCGGTGAAGAGCGTGATGA GGCTGTCTCCCCGATTAAAGAATGTCTTATCAAT AATTCCGATGAACTTCGACTGGACGTTTAAATC TGCCTCGCTACCTGACACTTACCAGCTCAGA TAACGCTGCTCAATGTATCATAATCAATTAAC TAACGCTGCTCAATGTATCATAATCAATTAC TAACGCTGCTCCAATGTACGCTAAAAAAA TTATATTCCGCCAGCAATAAATTATCAGAATTGC CCGTGCTACCTCCCGCCTGGAACTTGC TACAACACAATGAGTGATAGCTTCAGG TACAACACAATGAGTGAATAGC TACAACACAATGAGTGAATACAGGTT TACAACACAATGAGTGAATATCAGGTT TACAACACAATGAGTTATTGAAATATCAGGTT
	ω ω ο
	Shigella ipaH9.8
	Shigell

	MKITSTIIQTPFPFENNNSHAGIVTEPILGKLIGUG STAEIFEDVNDSSALYKKYDLIGNQYNEILEMAW QESELFNAFYGDEASVVIQYGGDVYLRMLRVPG TPLSDIDTADIPDNIESLYLQLICKLNELSIIHYDLN TGNMLYDKESESLFPIDFRNIYAEYYAATKKDKEI IDRRLQMRTNDFYSLLNRKYL*TYLLML*
	41
	[1-612]
TAACGAAATAGTCTCCTTACCATCGCTCCCACA GGCTCTTAAAAATCTCAGAGCGACCCGTAATTT CCTCACTGAGCTACCAGCATTTTCTGAGGAAA TAATCCCGTTGTCAGAGAGTATTTTTTGATAGA AATCAGATAAGTCATATCCCGGAAAGCATTCTTA ATCTGAGGAATGATGTTCCATGCTCTGCAGGCCT GCAAGGATTACCTTCCCATGCTCTGCAGGCCT GCAAGATACACTCTTCCCATGAGTGACGAGCC CGTGACAGCATCCTTCCCGGAAACAAACAGC CGTGACAGCATCCCATCGCCCCTGGCTGATGC CGTGACAGCATCCCATCGCCCCTGGCTGATGC CGTGACAGCATCCCATCGCCCCTGGCTGATGC CGTGACAGCATCCGTGAAACAAACAAACAA ACAGAAACCTCCATCGCATGCTTTTGAACAT GAGAGCATTCCGAAAACCAAACGATC CTGGAAAAACTCGTGAACGTTCGAACACTCGGAAAACCTCGGGACCTTTCCGAACAGCTTCGGAAACCTCTGCGGAGCTTCGA	ATGAAATAACATCTACCATTATTCAAACACCTTT TCCATTTGAGAATAATATCTCCATGCTGCTGGCTGGCTGG
	Ospo
	Shigella

	TATAA	AA
Table II: B	: Bait-prey interactions	ractions
1: Bait name	2: Bait nucleic	3: Prey name
	S	
Shigella ospB	_	prey44074 (JM5; prey44078) hJM5
1	1	prey67804 (LOC91851) hhypothetical proteinXP 041083
Shigella ospB	1	prey67806
	-	prey67810 (FBXO3 FBX3 DKFZp564B092 FBA) hFBXO3
	1	prey5237 (NONO NRB54 NMT55 P54NRB) hNONO
1	1	prey67661 (CAPN2 CANPL2 CANPML) hCAPN2
Shigella ospB	1	prey34730 (LMO4; prey34731) hLMO4
Shigella ospB	-	1 (ZIN; prey33142) hZIN
Shigella ospB	-	(LOC136773) hsimilar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE,
		PRECURSOR (HIBADH) (H.sapiens)
Shigella ospB	-	prey67608 (MGC4126) hMGC4126
1	1	prey67637 (LOC90706) hhypothetical proteinXP_033663
Shigella ospB	1	prey12713 (LMO2 RBTNL1 RHOM2 TTG2 RB1N2; prey12714) nLMO2 n116-2a/RB1N-2a
	1	prey67836 (MYO9A) hMYO9A
Shigella ospB	1	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey/01) nRANBP9 nRanbrw
	1	prey67844
Shigella ospB	1	prey67853
Shigella ospB	1	
Shigella ospD1	2	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey/01) nRANBP9 nRanbrin
	2	prey2492 (FLJ11026; prey2493) hFLJ11026
Shigella ospD1	2	prey67651 putative homolog of prey064241 - Mouse
	2	prey67653 putative homolog of prey067652 -
Shigella ospD1	2	prey67667 (PACSIN2) hPACSIN2
	2	prey67657 hUnknown (protein forMGC:16824)
Shigella ospD1	2	prey67501 (LOC51667) hLOC51667
	2	prey67678 (LOC90410) hhypothetical proteinXP_031534
	2	prey67578 (LOC121052) hhypothetical proteinXP_U35313
Shigella ospD1	2	prey67580 (DKFZp586i021) nUKFZp586i021

ospD1 2 ospC1 3	prey50427 (KIAA0419; prey50428) hKIAA0419 prey60427 (KIAA0419; prey50428) hKIAA0419 prey63765 (LIM; prey63767) hLIM prey67623 (LDB2 CLIM1) hLDB2 prey67623 (LDB2 CLIM2 NLI; prey7316) hLDB1 hCLIM2 prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey67630 (PREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (SYNCOILIN; prey20144) hSYNCOILIN prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67690 (TID1; prey48229) hTID1 prey67080 (TID1; prey48229) hTID1
ospD1 2 ospC1 3	prey63765 (LIM; prey63767) hLIM prey676523 (LDB2 CLIM1) hLDB2 prey67623 (LDB2 CLIM1) hLDB2 prey7315 (LDB1 CLIM2 NLI; prey7316) hLDB1 hCLIM2 prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey67601 (ATIP1 KIAA1027) hTLN1 prey67630 prey67630 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67643 (SYNCOILIN; prey20144) hSYNCOILIN prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67566 prey67567 prey67567 prey675690 (TID1; prey48229) hTID1 prey67822
ospD1 2 ospC1 3	prey67623 (LDB2 CLIM1) hLDB2 prey7315 (LDB1 CLIM2 NLI; prey7316) hLDB1 hCLIM2 prey7315 (LDB1 CLIM2 NLI; prey7316) hLDB1 hCLIM2 prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey67601 (ATIP1 KIAA1287 hTLN1 prey67630 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67643 (SYNCOILIN; prey20144) hSYNCOILIN prey67642 (ALDH3B2 PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67646 prey67648 (PON2) hTID1 prey67590 (TID1; prey48229) hTID1 prey50590 (TID1; prey48229) hTID1
ospD1 2 ospC1 3	prey7315 (LDB1 CLIM2 NLI; prey7316) hLDB1 hCLIM2 prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey53735 (TLN1 TLN KIAA1027) hTLN1 prey67630 prey67630 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67643 (SYNCOILIN; prey20144) hSYNCOILIN prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67266 prey67267 prey67287 prey67287 prey67287
ospD1 2 ospC1 3	prey67601 (ATIP1 KIAA1288 DKFZp586D1519 FLJ14295) hATIP1 prey53735 (TLN1 TLN KIAA1027) hTLN1 prey53735 (TLN1 TLN KIAA1027) hTLN1 prey67630 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67648 (PON2) hPON2 prey67266 prey67266 prey67267 prey67267 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey53735 (TLN1 TLN KIAA1027) hTLN1 prey53735 (TLN1 TLN KIAA1027) hTLN1 prey67630 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey67631 (FLJ21742) hFLJ21742 prey67631 (FLJ21742) hFLJ21742 prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67666 prey67266 prey67266 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey67630 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey67631 (FL)21742) hFL)21742 prey20143 (SYNCOILIN; prey20144) hSYNCOILIN prey1418 (NR1H2 UNR NER NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I prey67642 (ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67666 prey67266 prey67267 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey12665 (CREBL1 CREB-RP G13; prey12666) hCREBL1 hG13 prey67631 (FL)21742) hFL)21742 prey67631 (FL)21742) hFL)21742 prey20143 (SYNCOILIN; prey20144) hSYNCOILIN prey1418 (NR1H2 UNR NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I prey67642 (ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67266 prey67267 prey67267 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey67631 (FLJ21742) hFLJ21742 prey20143 (SYNCOILIN; prey20144) hSYNCOILIN prey1418 (NR1H2 UNR NER NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67266 prey67266 prey67267 prey67267 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey20143 (SYNCOILIN; prey20144) hSYNCOILIN prey1418 (NR1H2 UNR NER NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67266 prey67267 prey67267 prey67267 prey67267 prey67267 prey67267 prey67267
ospD1 2 ospD1 2 ospD1 2 ospC1 3	prey1418 (NR1H2 UNR NER NER-I RIP15 LXR-B; prey1419) hNR1H2 hNer-I prey67642 (ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67266 prey67266 prey67267 prey67267 prey67267 prey67267 prey67280 (TID1; prey48229) hTID1 prey9822
ospD1 2 ospC1 3	prey67642 (ALDH3B2 ALDH3B2-PENDING ALDH8) hALDH3B2 prey67648 (PON2) hPON2 prey67266 prey67267 prey50590 (TID1; prey48229) hTID1 prey9822
ospD1 2 ospC1 3	prey67648 (PON2) hPON2 prey67266 prey50590 (TID1; prey48229) hTID1 prey9822
ospC1 3	prey67266 prey67267 prey50590 (TID1; prey48229) hTID1 prey9822
ospC1 3 ospC1 5 ospC1	prey67267 prey50590 (TID1; prey48229) hTID1 prey9822
ospC1 3	prey50590 (TID1; prey48229) hTID1 prey9822
ospC1 3	prey9822
ospC1 3	
ospC1 3	prey67268
ospC1 3	prey67270
ospC1 3	prey67271 (STAT5B STAT5) hSTAT5B
ospC1 3	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 hRanBPM
ospC1 3 ospC1 3 ospC1 3 ospC1 3 ospC1 3 ospC1 3	prey3486 (PM5; prey3487) hPM5 hpM5
ospC1 3 ospC1 3 ospC1 3 ospC1 3 ospC1 3	
ospC1 3 ospC1 3 ospC1 3	prey67279
ospC1 3	prey67280
ospC1 3	prey49194 (KIAA0211; prey49195) hKIAA0211
2000	prey67287
	prey19931 (HEF1 CAS-L) hHEF1
Shigella ospC1 3	prey67290
Shigella ospC1 3	prey67291
3	prey67294
3	prey67296
ospC1 3	prey67299

Shigella ospC1	3	prey4637 (TAF2A BA2R CCG1 CCGS NSCL2 TAFII250; prey4638; prey4639) hTAF2A
Shigella ospC1	3	prey67316
Shigella ospC1	3	prey67318
1	3	prey7144 (IMMT P87/89 HMP; prey7145) hIMMT hp87/89
	3	prey67328 (TSC22) hTSC22
1	3	prey37430 (WASL N-WASP; prey37432) hWASL hN-WASP
Shigella ospC1	3	prey67351
Shigella ospC1	3	prey67353
Shigella ospC1	3	85 hHSPC272
	3	prey4411 (ZNF147 EFP TRIM25 Z147) hZNF147
1	3	prey2686 (VRP AD3; prey2687) hVRP
	3	prey67368 (LOC92609) hhypothetical proteinXP_053074
	3	prey67371
Shigella ospC1	3	prey4005 (KIAA0141; prey4006; prey8649; prey44107) nKIAA0141
Shigelia ospC1	3	prey67380
	3	prey3296 (FHOS; prey3297) hFHOS
Shigella ospC1	3	prey2108 (prey2101; prey2104; prey2107; prey2102; prey2103) nsimilar to COP9 (constitutive priorationally), subjunit 5(Arabidopsis, homolog) subunit 5 (H.sapiens)
		hCOPS5 hsimilar to COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 (H.sapiens) hCOPS5
		hsimilar to COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 (H.sapiens)
Shigella ospC1	3	prey67403
Shigella ospC1	3	prey67405
Shigella ospC1	3	prey14400 (prey14399; prey14401) hprotein phosphatase 5, catalyticsubunit nerroc inerroc
Shigella ospC1	3	prey50029
Shigella ipaD	4	prey67563 (PRSC1) hPRSC1
Shigella ipaD	4	prey2109 (COPS5 JAB1 SGN5 MOV-34; prey2110) nCOPS5 n38 KDa Mov341101109
Shigella ipaD	4	prey25185 hHSPC272
ı.	4	prey53990 (TNFRSF1A CD120a TNF-R TNF-R-I INF-R55 INFAR INFRED INFR 1935-R p35) IIINI INSTITUTION
Shigella ipaD	4	prey9120 (VIM; prey9122) hVIM hvimentin
Shigella ipaD	4	prey67571
	4	prey67572
Shigella ipaD	4	prey65696 (KARS KIAA0070; prey65697) hKARS nLysyi tRNASynmetase
	4	prey8889 (PLCB3) hPLCB3
Shigella ipaD	4	prey700 (RANBP9 RANBPM KANBP9-PENDING; prey701) IIRANDP 9 IINAIID W

Shinella inal	4	prev2694 (INDO IDO; prey2696; prey2693) hINDO hINDO
1	4	ILC)
1	4	prey67574
Shigella ipaC	5	prey67509 (POLR2A RPOL2 POLR2 POLRA hRPB220 hsRPB1 RPU2 RPIILS RPBN1 RPB1) IIPULR2A
Shigella ipaC	5	
ı	5	
1	2	
Shigella ipaC	5	prey4458 (RRBP1 ES130 ES/130; prey4459) nRRBP1 nES/130
Shigella ipaC	2	prey67522
Shigella ipaC	2	prey527 (CLTC CLTCL2 KIAA0034; prey528) hCLTC hKIAA0034
Shigella ipaC	5	prey53735 (TLN1 TLN KIAA1027) hTLN1
Shigella ipaC	2	prey53735 (TLN1 TLN KIAA1027) hTLN1
Shigella ipaC	5	prey67546 (LOC128116) hsimilar to phosphodiesterase 4D Interacting protein (Inyoniegalin) (11.3aprens)
	5	prey4671 (KIAA0454) hKIAA0454
	2	
	2	prey8889 (PLCB3) hPLCB3
1	5	prey11375 (HSPBP1; prey11376) hHSPBP1 hHsp70 binding proteinHSpBP1
Shigella ipaC	2	
Shigella ipaC	5	
Shigella ipaC	5	
	5	
Shigella ipaC	5	
	5	prey5814 (USP9X DFFRX) hUSP9X
Shigella ipaC	5	Z . I
Shigella ipaC	5	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey/01) nRANBP9 nRanbriw
1	5	prey67481 (GDBR1 GBDR1) hGDBR1
Shigella ipaC	5	prey67488 (LOC126257) hsimilar to putative (H.sapiens)
	2	prey51967 (UBQLN1 DSK2 PLIC-1 DA41 XDRP1) hUBQLN1
	2	
Shigella ipaC	5	prey323 (CSH1 CSMT CSA PL; prey324; prey325) hCSH1
Shigella ipaC	5	prey67495
Shigella ipaC	5	prey67506 (LOC126083) hdynamin2
Shigella ipaC	5	prey4578 (PSAP SAP1 GLBA; prey5664) nPSAP nGLBA
Shigella ipaC	5	prey1135 (PSMD1 P112 S1; prey1136) nPSMD i riprotedsonie suburinți 12

Shigella ipaC	5	prey67465 (COL4A2 FLJ22259) hCOL4A2
Shigella ipaC	2	
Shigella ipaC	5	prey3599 (TRIP12 KIAA0045; prey3600) hTRIP12 hKIAA0045
Shigella ipaH9.8	9	prey67717
1	9	prey700 (RANBP9 RANBPM RANBP9-PENDING; prey701) hRANBP9 nRanBPM
	9	prey67718 (KIAA1715) hKIAA1715
1	9	prey2530 harrestin, beta1
	9	prey67731 (LOC126896) hsimilar to Gene 33/Mig-6 (H.Sapiens)
	9	prey7155 (CSH2 CSB) hCSH2
1	9	prey1687 (DCTN1) hDCTN1
	9	(FLJ10618) hFLJ10618
	9	prey2694 (INDO IDO; prey2696; prey2693) hINDO hINDO
1	9	prey67740
ı	9	prey67703 (PPP2R4 PTPA) hPPP2R4
	9	prey67741
1	9	prey67742 (FLJ20313) hFLJ20313
	9	prey67339 (MMP19 RASI-1 MMP18) hMMP19
1	9	prey67337 (MMP19 RASI-1 MMP18) hMMP19
1	9	prey67746 (FBXO25 FBX25) hFBXO25
	9	prey54430 (PSG4 PSG9) hPSG4
	9	prey67749
ł .	9	prey67751
	9	prey8739 (MLL2 ALR; prey8742) hMLL2 hALR
Shigella ipaH9.8	9	prey18232 (CCT3 TRIC5 CCTG; prey18233) hCC13 hCctg
Shigella ipaH9.8	9	prey66739 (EIF2B1 EIF2B EIF-2B) hEIF2B1
ı	9	prey67769 (PP2135 FLJ00041) hPP2135
Shigella ipaH9.8	9	prey13613 (KIAA0970) hKIAA0970
	9	prey3337 (LMNA LMN1 EMD2 FPL LFP LDP1 FPLD CIMD1A; prey14199) filmina
Shigella ipaH9.8	9	prey67774 (LOC119758) hsimilar to REGULATOR OF PRESYNAPTIC ACTIVITY AEA-3 (FI.34ptens)
Shigella ipaH9.8	9	prey67776
	9	prey4758 (DKFZP761L0424 KIAA1217) hDKFZP/61L0424
	9	prey67781 putative homolog of prey046760 - Mouse Fmnl
	9	prey2109 (COPS5 JAB1 SGN5 MOV-34; prey2110) nCOPS5 fise KD4 MOV34ficitions
Shigella ipaH9.8	9	prey4060 (KIAA0155; prey4061; prey4062) InklAA0133

Shinella inaH9.8	8		prey49284 (SLC7A8 LAT2) hSLC7A8
	Ť		prey67686
1	8		prey66872 (MRPS9) hMRPS9
1	9		prey67690 (RRP4) hRRP4
Shigella ipaH9.8	9		prey67695 (ATP6N1B RDRTA2 RTA1C VPP2 RTADR) hATP6N1B
Shigella ipaH9.8	9 8.		prey67336 (MMP19 RASI-1 MMP18) hMMP19
	8.		prey6299 (KIAA0335; prey6300) hKIAA0335
Shigella ipaH9.8	8.		prey6586 (FLNA ABPX ABP-280 FLN FLN1 NHBP; prey6587) hFLNA
			prey56789 (ALDH4 P5CDH; prey56791) hALDH4 hP5CDh
	8.		prey67711
1	8.		prey2118 (RNF2 dinG Bap-1; prey2119) hRNF2 hring finger proteinBAP-1
Shigella ipaH9.8	8.		prey3596 (DDX15 HRH2 DBP1; prey3597) hDDX15 hATP-dependent RNA helicase#4b
Shigella ipaH9.8	8.		prey666 (RANBP16 KIAA0745; prey667; prey665; prey9721) hKANBP16 nKAN binding protein to incandr to
	-		
Shigella ospG			prey3917 (BTBD2 FLJ20386; prey3920; prey3918; prey3921; prey3922; prey3919) nb1bD2
Shigella ospG	7		prey63632 (ZNF189; prey63789) hZNF189
Shigella ospG	7		prey2109 (COPS5 JAB1 SGN5 MOV-34; prey2110) hCOPS5 h38 kDa Mov34nomolog
Shigella ospG	_		prey54201 (UBE2D3 UBCH5C; prey54202) hUBE2U3 hUBCH5C
Shigella ospG	7		prey1922 (DLST DLTS; prey1923) hDLST hE2K
Shigella ospG	_		
Shigella ospG	7		prey67314 (UBE2L6 UBCH8 RIG-B) hUBE2L6
ı	7		prey67435 hUnknown (protein forMGC:3432)
1	_		prey67443 (FLJ11807) hFLJ11807
Shigella ospG	7		prey67317 (KIAA1485) hKIAA1485
Shigella ospG	7		mı
Shigella ospG			prey700 (RANBP9 RANBPM RANBP9-PENDING; prey/01) nRANBP9 nRanBPM
Shigella ospG			prey67411 (UBE2E3 UBCH9) hUBE2E3
Shigella ospG			prey67423
			prey67298
Shigella ospG	-		prey67464
Shigella ospG			prey67320
Shigella ospG	-		prey67321
Shigella ospG			prey35777 (PSG2 PSBG2 PSGGB; prey35778) hPSG2 hPSG1
Shigella ospG		_	prey67327 (AKAP13 HT31 BRX) hAKAP13

Shigella ospG 7 prey50598 (PE Shigella ospG 7 prey67364 Shigella ospG 7 prey67367 Shigella ospG 7 prey67369 Shigella ospG 7 prey67369	PEX10 NAI D: prev50599) hPEX10 hperoxisome assembly proteinPEX10
7 7 7	
7 7	7364
7	7367
7	7369
	prey67372 (CD63 MLA1 ME491) hCD63
7	77379
7	prey67381 (LOC131541) hhypothetical proteinXP_059524

,		1-LIADOOSE451ADOOSE45 Homo sanians mRNA for RanBPM, complete cds.
ospB	_	gulybougo 19/bougo 19 10mio suprime many control from 7014 nd 5 complete sequence
gdso	-	gb AC005091 AC005091 Homo saplens BAC Glore CTA-310CT1 IOH / pt4-pt3, compress sequence.
OSDB	-	gb AF117888 AF117888 Homo sapiens myosin-IXa mRNA, complete cds.
OSDB	-	gb AF141347 AF141347 Homo sapiens hum-a-tub2 alpha-tubulin mRNA, complete cds.
OSOB	-	gb AF176702 AF176702 Homo sapiens F-box protein FBX3 mRNA, partial cds.
Baso	-	gblAF177198 AF177198 Homo sapiens talin mRNA, complete cds.
Basa	-	gbjAF212940JAF212940 Homo sapiens zinedin (ZIN) mRNA, complete cds.
gaso	-	gblAF257211[AF257211 Homo sapiens LMO2b splice variant (LMO2) mRNA, complete cds.
ospB	-	gb AJ005897 HSA005897 Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
ospB	_	gb AK024239 AK024239 Homo sapiens cDNA FLJ14177 fis, clone NT2RP2003161.
ospB	-	gb AL049176 HS141H5 Human DNA sequence from clone 141H5 on chromosome Xq22.1-23. Contains parts of a novel chordin LIKE protein with von Willebrand factor type C domains. Contains ESTs, STSs and GSSs, complete
		sequence.
ospB	-	gb AL122043 HSM801240 Homo sapiens mRNA; cDNA DKFZp566G1424 (from clone DKFZp566G1424).
gdso	1	gblAL442166IHSMX1A Homo sapiens chromosome 21 from 5 PACs and 5 Cosmids map 21q22.2,U213349-MA1,
ospB	-	gb AP002026 AP002026 Homo sapiens genomic DNA, chromosome 4qzz-qz4, clone:4z3nz I, complete sequence:
ospB	-	gblD21260 HUMORFEA Human mRNA for KIAA0034 gene, complete cds.
OSpB	-	gb L14599 HUMPSFHOMO Human mRNA, complete cds.
ospB	-	gblL28809 HUMAAE Homo sapiens dbpB-like protein mRNA, complete cds.
ospB	1	
ospB	-	gb U24576 U24576 Homo sapiens breast tumor autoantigen (LMO4) mRNA, complete cds.
gdso	-	gb X61118 HSTTG2 Human TTG-2 mRNA for a cysteine rich protein with LIM motif.
ospD1	2	gb AB007879 AB007879 Homo sapiens KIAA0419 mRNA, complete cds.
ospD1	2	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
ospD1	2	gb/AB016485/AB016485 Homo sapiens mRNA for LIM homeobox protein coractor (CLIM-2), complete cus.
ospD1	2	
ospD1	2	gb/AB033114/AB033114 Homo sapiens mRNA for KIAA1288 protein, partial cds.
ospD1	2	gb/AC003108/HUAC003108 Human Chromosome 16 BAC clone CII 30/ Shr-32/ 024, Williplete Sequence:
ospD1	2	gb/AC008764/AC008764 Homo sapiens chromosome 19 clone CTD-3222D19, witiplete sequence:

	6	Lative on ten 11A En 01 En 1 Homo saniens paraoxonase (PON2) mRNA, complete cds.
1.0dso	7	golfal of 100 100 100 100 100 100 or promise forming forming related protein (Fr1) mRNA, complete cds.
ospD1	2	go/Ar-U00400/Ar-U00400 Mus IIInscullus yiilyingyk again a sanaga aga
ospD1	7	gb AF061258 AF061258 Homo sapiens LIM protein mknA, complete cus.
ospD1	2	gb/AF068651/AF068651 Homo sapiens LIM-domain binding factor CLIM1 (CLIM1) mKNA, complete cus.
ospD1	2	gb AF128536 AF128536 Homo sapiens cytoplasmic phosphoprotein PACSINZ mKNA, complete cds.
ospD1	2	gb AF155099 AF155099 Homo sapiens NY-REN-18 antigen mRNA, complete cds.
ospD1	2	gb AF177198 AF177198 Homo sapiens talin mRNA, complete cds.
ospD1	2	gb AF265342 AF265342 Homo sapiens chromosome 8 map 8p BAC 2053N22, complete sequence.
ospD1	2	gb AK001888 AK001888 Homo sapiens cDNA FLJ11026 fis, clone PLACE1004104.
ospD1	2	gb AL121808 CNS01DSJ Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC C-2313013 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
ospD1	2	
ospD1	2	gb B88348 B88348 CIT-HSP-2063N18.TFB CIT-HSP Homo sapiens genomic cione Zuosin Io, DINA sequerice.
ospD1	2	
ospD1	2	gb M63960 HUMPRPHOS1 Human protein phosphatase-1 catalytic subunit mRNA, complete cds.
ospD1	2	gb U07132 HSU07132 Human steroid hormone receptor Ner-I mRNA, complete cds.
ospD1	2	gb U31903 HSU31903 Human CREB-RP (creb-rp) mRNA, complete cds.
ospD1	2	gb U37519 HSU37519 Human aldehyde dehydrogenase (ALDH8) mKNA, complete cds.
ospD1	2	gb X65873 HSKHCMR H.sapiens mRNA for kinesin (heavy chain).
ospD1	2	gb X65873 HSKHCMR H.sapiens mRNA for kinesin (heavy chain).
ospD1	2	gb X65873 HSKHCMR H.sapiens mRNA for kinesin (heavy chain).
Dadi	4	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
ipaD	4	gb AF161390 AF161390 Homo sapiens HSPC272 mRNA, partial cds.
ipaD	4	gb/AF177198/AF177198 Homo sapiens talin mRNA, complete cds.
ipaD	4	gblD32053 D32053 Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds.
IpaD	4	gb D55696 D55696 Homo sapiens mRNA for cysteine protease, complete cds.
IpaD	4	gb M14144 HUMVIM Human vimentin gene, complete cds.
Dadi	4	
Dedi	4	gb M63121 HUMTNFRC Human tumor necrosis factor receptor (TNF receptor) mixINA, complete cus.
ipaD	4	gblU70734 HSU70734 Homo sapiens 38 kDa Mov34 homolog mkNA, complete cus.
IpaD	4	gb Z26649 HSPPLCB3 H.sapiens mknA for phospitolipase C-b3.

Dadi	4	Igb Z26649 HSPPLCB3 H.sapiens mRNA for phospholipase C-b3.
ipaC	5	gb/AB002366/AB002366 Human mRNA for KIAA0368 gene, partial cds.
ipaC	5	gb/AB002533/AB002533 Homo sapiens mRNA for Qip1, complete cds.
ipaC	5	gb AB007923 AB007923 Homo sapiens mRNA for KIAA0454 protein, partial cds.
ipaC	2	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
ipaC	5	gblAB018271 AB018271 Homo sapiens mRNA for KIAA0728 protein, partial cds.
ipaC	2	gblAB020335JAB020335 Homo sapiens Pancreas-specific TSA305 mRNA, complete cds.
ipaC	5	gblAB023224JAB023224 Homo sapiens mRNA for KIAA1007 protein, partial cds.
ipaC	2	gb AB029290 AB029290 Homo sapiens mRNA for actin binding protein ABP620, complete cds.
ipaC	2	gb AB046026 AB046026 Macaca fascicularis brain cDNA, clone: OccE-16688.
ipaC	5	gb AC003991 AC003991 Human BAC clone CTB-167B5 from 7q21, complete sequence.
ipaC	2	gb AC005578 AC005578 Homo sapiens chromosome 19, cosmid F20887, complete sequence.
ipaC	5	gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	5	gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	5	gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	5	gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds.
ipaC	5	gb AF100153 AF100153 Homo sapiens connector enhancer of KSR-like protein CNK1 mKNA, complete cds.
ipaC	2	gb AF176069 AF176069 Homo sapiens ubiquilin mRNA, complete cds.
ipaC	2	gb AF176069 AF176069 Homo sapiens ubiquilin mRNA, complete cds.
ipaC	5	gb AF176796 AF176796 Homo sapiens putative glialblastoma cell differentiation-related protein (GBUR1) mKNA,
		complete cds.
ipaC	ഹ	gb AF176796 AF176796 Homo sapiens putative gliatorastorità dell'uniterioritation dell'accompany (2007). Complete cds.
ipaC	လ	gb AF176796 AF176796 Homo sapiens putative glialblastoma cell differentiation-related protein (GBUR1) mRNA, complete cds.
ipaC	2	gb AF177198 AF177198 Homo sapiens talin mRNA, complete cds.
ipaC	5	gb AF177198 AF177198 Homo sapiens talin mRNA, complete cds.
ipaC	ည	gb/AF187859/AF187859 Homo sapiens Hsp70 binding protein HspBP/2 mRNA, complete cds.
ipaC	2	gb/AF189009/AF189009 Homo sapiens ubiquitin-like product Chap1/DSKZ mKNA, complete cus.
ipaC	2	gb/AK000982/AK000982 Homo sapiens cDNA FLJ10120 its, clone HEMBA (002003).
ipaC	5	gb D21260 HUMORFEA Human mRNA for KIAAUU34 gene, complete cos.
ipaC	5	gb D28476 HUMKG1C Human mKNA for KIAAUU45 gene, complete cos.

Jeui	3	InhID44466ID44466 Homo sapiens mRNA for proteasome subunit p112, complete cds.
Cedi	2	
Dag	2	
ipaC	5	
ipaC	5	gblL36983 HUMDNM Homo sapiens dynamin (DNM) mRNA, complete cds.
ipaC	5	
ipaC	2	
ipaC	5	gblM24766 HUMCOL4A2P Human (clone pHAIV2-12) alpha-2 collagen type IV (COL4A2) mKNA, 3 end.
ipaC	5	gb M81355 HUMSPHINO Homo sapiens sphingolipid activator proteins 1 and 2 processed mutant mKNA, complete cos.
ipaC	သ	gb U02389 HSU02389 Human hLON ATP-dependent protease mRNA, nuclear gene encoding mitochondrial protein, complete cds.
ipaC	5	
ipaC	5	gb X05610 HSC4A2 Human mRNA for type IV collagen alpha (2) chain.
ipaC	5	gb X63564 HSRPIILS H.sapiens mRNA for RNA polymerase II largest subunit.
ipaC	5	gb X98296 HSUBIQHYD H.sapiens mRNA for ubiquitin hydrolase.
ipaC	5	gb Z26649 HSPPLCB3 H.sapiens mRNA for phospholipase C-b3.
ipaH9.8	9	dbj AB001636.1 AB001636 Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds
ipaH9.8	9	dbj AB002333.1 AB002333 Human mRNA for KIAA0335 gene, complete cds
ipaH9.8	9	dbj AB008515.1 AB008515 Homo sapiens mRNA for RanBPM, complete cds
ipaH9.8	9	dbjjAB023187.1JAB023187 Homo sapiens mRNA for KIAA0970 protein, complete cds
ipaH9.8	9	dbjjAB033043.1JAB033043 Homo sapiens mRNA for KIAA1217 protein, partial cds
іраН9.8	9	dbjjAK001451.1JAK001451 Homo sapiens cDNA FLJ10589 fis, clone NT2RP2004389, weakly similar to PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR
8.6Hedi	9	dbj AK024449.1 AK024449 Homo sapiens mRNA for FLJ00041 protein, partial cds
ipaH9.8	9	. 1 D63875 Human mRNA for KIAA0155 gene, complete cds
іраН9.8	9	emb AL034405.16 HS537K23 Human DNA sequence from clone RP4-537K23 on chromosome Xq25-26.1, complete sequence [Homo sapiens]
іраН9.8	9	emb AL034417.14 HS215D11 Human DNA sequence from clone 215D11 on chromosome 1p36.12-36.33 Contains a gene for a RNA-binding protein regulatory subunit, a gene similar to rat gene 33, a pseudogene similar to PLA-X, ESTs, STSs, GSSs and CpG islands, complete sequence [Homo sapie
іраН9.8	O	emb AL050313.6 HSBK754D9 Human DNA sequence from clone CTA-754D9 on chromosome 22 Contains GSSs, complete sequence [Homo sapiens]

& oHeari	e e	Jembial 117448 11HSM800958 Homo sapiens mRNA; cDNA DKFZp586B1417 (from clone DKFZp586B1417); partial cds
a office:	٥	emblai 137068 10141 137068 Hilman DNA sequence from clone RP11-165P4 on chromosome 9q34.11-34.13, complete
pana.o	o	
ipaH9.8	9	emb X53416.1 HSABP280 Human mRNA for actin-binding protein (filamin) (ABP-280)
ipaH9.8	9	emb X73478.1 HSPTPAA H.sapiens hPTPA mRNA
ipaH9.8	9	emb X74801.1 HSHUMAPC H.sapiens Cctg mRNA for chaperonin
ipaH9.8	9	emb X95648.1 HSEIF2BAS H.sapiens mRNA for eIF-2B alpha subunit
ipaH9.8	9	gb AC005392.1 AC005392 Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence
ipaH9.8	ဖ	gbjAC005833.1jAC005833 Homo sapiens 12p13.3 BAC RPCI11-234B24 (Roswell Park Cancer Institute Human BAC Library) complete sequence
ipaH9.8	9	gb[AC005881.3]AC005881 citb_79_e_16, complete sequence [Homo sapiens]
ipaH9.8	9	gblAC020663.1lAC020663 Homo sapiens chromosome 16 clone RPCI-11_127l20, complete sequence
ipaH9.8	9	gblAF006466.1 JAF006466 Mus musculus lymphocyte specific formin related protein (Fr1) mRNA, complete cds
ipaH9.8	9	gb AF010404.1 AF010404 Homo sapiens ALR mRNA, complete cds
ipaH9.8	9	gblAF064729.1 AF064729 Homo sapiens RAN binding protein 16 mRNA, complete cds
ipaH9.8	9	gb AF084940.1 AF084940 Homo sapiens beta-arrestin 1B mRNA, complete cds
ipaH9.8	9	gb AF135159.1 AF135159 Homo sapiens GMP reductase mRNA, complete cds
ipaH9.8	9	gblAF139184.1 AF139184 Homo sapiens Sec31 protein mRNA, complete cds
ipaH9.8	9	gb AF141327.1 AF141327 Homo sapiens ring finger protein BAP-1 mRNA, complete cds
іраН9.8	9	gb AF171669.1 AF171669 Homo sapiens glycoprotein-associated amino acid transporter LAT2 (LAT2) mRNA, complete cds
ipaH9.8	9	gblAF174605.1 AF174605 Homo sapiens F-box protein Fbx25 (FBX25) mRNA, partial cds
ipaH9.8	9	gb AF207661.1 AF207661 Homo sapiens sodium bicarbonate cotransporter-like protein mRNA, partial cds
іраН9.8	9	gb AF245517.1 AF245517 Homo sapiens vacuolar proton pump 116 kDa accessory subunit (ATP6N1B) mKNA, complete cds, alternatively spliced
іраН9.8	g	gb AF249874.1 AF249874 Homo sapiens vacuolar proton pump 116 kDa accessory subunit gene, exon 3 and 5' untranslated region, partial sequence
ipaH9.8	9	gbjJ00118.1jHUMPLB Human placental lactogen hormone (PL-4) mRNA, complete cds
ipaH9.8	9	gb L14283.1 HUMPROKINC Human protein kinase C zeta mRNA, complete cds
ipaH9.8	9	
іраН9.8	9	gblM13451.1lHUMLAMC Human lamin C mRNA, complete cds
ipaH9.8	9	gblM21616.1 HUMPDGFR Human platelet-derived growth tactor (PDGF) receptor mKNA, complete cas

8 GHedi	9	gb M32053.1 HUMH19 Human H19 RNA gene, complete cds
ipaH9.8	9	gbiM34455.1IHUMIGIIDO Human interferon-gamma-inducible indoleamine 2,3-dioxygenase (IDO) mRNA, complete cds
ipaH9.8	9	
ipaH9.8	9	gb M98478.1 HUMTGH1A Human transglutaminase mRNA, complete cds
ipaH9.8	9	
іраН9.8	9	refINM_014285.1 Homo sapiens homolog of Yeast RRP4 (ribosomal RNA processing 4), 3-5-exonbonuclease (RRF4), mRNA
ipaH9.8	9	refINM_017762.1 Homo sapiens hypothetical protein FLJ20313 (FLJ20313), mRNA
ipaH9.8	9	ref[NM_018155.1 Homo sapiens hypothetical protein FLJ10618 (FLJ10618), mRNA
9dso	7	gb AB008515 AB008515 Homo sapiens mRNA for RanBPM, complete cds.
9dso	7	gb/AB013818/AB013818 Homo sapiens PEX10 mRNA for peroxisome biogenesis ractor (peroxin) 10, complete cus.
Sdso	7	gb AB033054 AB033054 Homo sapiens mRNA for KIAA1228 protein, partial cds.
OsbG		gb AB033054 AB033054 Homo sapiens mRNA for KIAA1228 protein, partial cds.
9dso	7	gb AB040918 AB040918 Homo sapiens mRNA for KIAA1485 protein, partial cds.
9dso	7	gb AC005281 AC005281 Homo sapiens PAC clone RP4-722F20 from 7q31.1-q31.3, complete sequence.
9dso	7	gbl/AE003603/AE003603 Drosophila melanogaster genomic scattoid 142000013385043 section 4 of 6, complete
		Sequence.
ospG	_	gplArtosousplartosous Figure sariens KDP/4k-1 profein mRNA complete cds.
Sdso		gplAFU351Z1/AFU351Z1 HOING Septembrianiting conjugation enzyme RIG-B mRNA, complete cds.
Sdso	7	gb AF061/36 AF061/36 Homo sapiens upiquiuli-cuijugaunig enizyme ruc Enimary, compressione
9dso	7	gb AF085362 AF085362 Homo sapiens Upciviz IIIIRINA, Collipse e cus.
9dso	7	gb AF104913 AF104913 Homo sapiens eukaryotic protein synutesis illination liatury, comprete cast.
9dso	7	anison
9dso		gb AJ000519 HSUBICONJ Homo sapiens mRNA for ubiquitin-conjugating enzyme UbcH/.
9dso	7	gb AK000393 AK000393 Homo sapiens cDNA FLJ20386 fis, clone KAIA4184.
9dso	7	gb AK001311 AK001311 Homo sapiens cDNA FLJ10449 fis, clone N12KP1000347, filgrily sliffliar to number 2 appears conjugating enzyme UbcH5B mRNA.
9dso	7	gb/AL050321/HSJ717M23 Human DNA sequence from clone RP4-717M23 on chromosome 20, complete sequence.

						C C C
1: Bait name	2: Bait	3: Prey name	<u>c</u>	5: SID nucleic acid sequence	6: SID amino-acid	amino-acid //: SiD amino-acid sequence
	nucleic					
	SFO		eic			
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		acid			
			<u>□</u>			
0.1.2.10	,	14074	2	CTTCAGCCACGACTCCTCCTTCCTGCGCT	216	FSHDSSFLCASSDKGTVHIFAL
Snigelia		prey440/4	2	TCAGTGATAAGGGTACTGTCCATATCTTTGC		KDTRLNRRSALARVGKVGPMI
adso				TOTOAAGATACCGCCTCAACCGCCGCTCC		GQYVDSQWSLASFTVPAESA
				ACCUTAGE TEGE GEORGE GEORGE GEORGE		CICAFGRNTSKNVNSVIAICVD
				ATGATTGGGCAGTACGTGGACTCTCAGTGGA		GTFHKYVFTPDGNCNREAFD
				GCCTGGCGAGCTTCACTGTGCCTGCTGAGTC		VYLDICDDDDF*
				AGCTTGCATCTGCGCCTTCGGTCGCAATACT		
				TCCAAGAACGTCAACTCTGTCATTGCCATCTG		
				CGTAGATGGGACCTTCCACAAATATGTCTTCA		
				CTCCTGATGGAAACTGCAACAGAGAGAGGCTTT		
				CGACGTGTACCTTGACATCTGTGATGATGAT		
				GACTITIAA		
Chimplio	-	Prov67804	16	GACCAGCAAGTCTTGCGAGTACAATGGGACA	217	TSKSCEYNGTTYQHGELFVAE
Snigella	_	pieyor out	2	ACTTACCAACATGGAGAGCTGTTCGTAGCTG		GLFQNRQPNQCTQCSCSEGN
osbe				AAGGCTCTTTCAGAATGGGCAAGGCAATGA		VYCGLKTCPKLTCAFPVSVPD
				ATOMOGRACION OF THE TABLE A COMPANY OF THE TA		SCCRVCRGDGELSWEHSDG
				A GCACCCAG GCAGC G T CGCACCG V V CC		DIFROPANREARHSYHRSHYD
				GIGIALIGI GGI CI CANGACI I COCCOS SECTI		PPPSRQAGGLSRFPGARSHR
				COTOCTOCTOCTATGCAGAGGAGATGGAG		GALMDSQQASGTIVQIVINNKH
				AACTGTCATGGGAACATTCTGATGGTGATATC		KHGQVCVSNGKTYSHGESWH
				TTCCGGCAACCTGCCAACAGAGAAGCAAGAC		PNLRAFGIVECVLCTCNVTKQ
				ATTOTACCACCACCACCACTATGATCCTCACTATGATCCTCCA		ECKKIHCPNRYPCKYPQKIDG
				CCAAGCCGACAGGCTGGAGGTCTGTCCCGC		KCCKVCPGKKAKELPGQSFD
				TTTCCTGGGGCCAGAGTCACCGGGGGAGCT		NKGYFCGEETMPVYESVFME
				CTTATGGATTCCCAGCAAGCATCAGGAACCA		DGETTRKIALETERPPQVEVH
				TTGTGCAAATTGTCATCAATAACAAACACAAG		WYTIRKGILQHFHIEKISKRMF
				CATGGACAAGTGTGTGTTTCCAATGGAAAGA		EELPHFKLVTRTTLSQWKIFTE

				CCTATTCTCATGGCGAGTCCTGGCACCCAAA CCTCCGGGCATTTGGCATTGTGGAGTGTGTG CTATGTACTTGTAATGTCACCAAGCAGAGTG TAAGAAAATCCACTGCCCCAATCGATACCC TGCAAGTTCCTCAAAAAATAGACGGAAAATG CTGCAAGGTGTCCTCAAAAAATAGACGGAAAATG CTGCAAGGTGTCCTCAAAAAATAGACGAAAAG GAACTTCCAGGCCAAGGTTTTGACAAAA GAACTTCTGCGGGGAAGAAAG GCTACTTCTGCGGGGAAGAACGATGCCTGT GTATGAAAAATAGCACTGGAGATGGAG ACCACCTCAGGTAGAGGTCCAGATGAA TTGAAAAATAGCATTCTCCAGCACTTCCATA TTGAGAAGGTTTTCAGGGAGA ACCCTGAAGGCATTCTCCAGCACTTCAAGG GACTCCTCACTTCAAGGTCTTCCAGGAACA ACCCTGAAGCTCAGAGATCTTCAAGG GAGAAGCTCAGAACAGAGATCTTCAAGG TCGTGTATGCAGAACAGAGATTTA GTCAAGGTTTTAA		GEAQISQMCSSRVCRTELEDL VKVLYLERSEKGHC*
Shigella ospB		prey67806	17	IGACCAGCCTGGTNANC NGGATGTNGTGTANCTG CATGATGACTTNTGGGA CGTTNTGNNNCGTNGTT CNTANGNTGTGNNACGA TAGGACCTGCNGTNTG GAGNTTNNTTAGGGGG AATNTGGGACTCTTAAG TTNTNGNNAAGAA	ω	XXLXXTSLVXLPGXTGCXVXV LCACHDDXWELXPSRXXXVV GXXPPXXVXRRLXFAKDLXXA ASXGEXXLGGXLXLKXWDS*V XXXVFXXK
Shigella ospB	-	prey67810	18	GGCGCCATGGAGACCGAGACGCCCCCT 219 GACCCTAGAGTCGCTGCCCCCCCTG CTCCTCATCTTATCCTTTTTGGACTATCGGGA TCTAATCAACTGTTGTTATGTCAGTCGAAGAC TTAGCCAGCTATCAAGTCATGATCGCTGTG GAGAAGACATTGCAAAAAATACTGGCTGTG CTGAGGAAGAAAACACAGGAGATCAGTG	<u>o</u>	AAMETETAPLTLESLP1DPLLLI LSFLDYRDLINCCYVSRRLSQL SSHDPLWRRHCKKYWLISEEE KTQKNQCWKSLFIDTYSDVGR YIDHYAAIKKAWDDLKKYLEPR CPRMVLSLKEGAREEDLDAVE AQIGCKLPDDYRCSYRIHNGQ

				TTGGAAATCTCTTCATAGATACTTACTGTG		KI VVPGI I GSMAI SNHYRSFD
				ATGTAGGAAGATACATTGACCATTATGCTGCT		LLDVDTAAGGFQQRQGLKYC
				ATTAAAAAGGCCTGGGATGATCTCAAGAAATA		LPLTFCIHTGLSQYIAVEAAEG
				TTTGGAGCCCAGGTGTCCTCGGATGGTTTTA		RNKNEVFYQCPDQMARNPAA
				TCTCTGAAAGAGGGTGCTCGAGAGGAAGACC		IDMFIIGATFTDWFTSYVKNVV
				TCGATGCTGTGGAAGCGCAGATTGGCTGCAA		SGGFPIIRDQIFRYVHDPECVA
				GCTTCCTGACGATTATCGATGTTCATACCGAA		TTGDITVSVSTSFLPELSSVHP
				TTCACAATGGACAGAAGTTAGTGGTTCCTGG		PHYFFTYRIRIEMSKDALPEKA
				GTTATTGGGAAGCATGGCACTGTCTAATCAC		CQLDSRYWRITNAKGDVEEV
				TATCGTTCTGAAGATTTGTTAGACGTCGATAC		QGPGVVGEFPIISPGRVYEYT
				AGCTGCCGGAGGATTCCAGCAGAGACAGGG		SCTTFSTTSGYMEGYYTFHFL
				ACTGAAATACTGTCTCCCTTTAACTTTTTGCA		YFKDKIFNVAIPRFHMACPTFR
				TACATACTGGTTTGAGTCAGTACATAGCAGTG		VSIARLVS*
		-		GAAGCTGCAGAGGGCCGAAACAAAAATGAAG		
				TTTTCTACCAATGTCCAGACCAAATGGCTCGA		
				AATCCAGCTGCTATTGACATGTTTATTATAGG		
				TGCTACTTTTACTGACTGGTTTACCTCTTATG		
				TCAAAAATGTTGTATCAGGTGGCTTCCCCATC		•
				ATCAGAGACCAAATTTTCAGATATGTTCACGA		
				TCCAGAATGTGTAGCAACAACTGGGGATATT		
				ACTGTGTCAGTTTCCACATCGTTTCTGCCAGA		
				ACTTAGCTCTGTACATCCACCCCACTATTTCT		
				TCACATACCGAATCAGGATTGAAATGTCAAAA		
				GATGCACTTCCTGAGAAGGCCTGTCAGTTGG		
				ACAGTCGCTATTGGAGAATAACAAATGCTAA		
				GGGTGACGTGGAAGAAGTTCAAGGACCTGG		
				AGTAGTTGGTGAATTTCCAATCATCAGCCCA		
				GETCGGGTATATGAATACACAAGCTGTACCA		
			,	CATTCTCTACAACATCAGGATACATGGAAGG		
				ATATTATACCTTCCATTTTCTTTACTTTAAAGA		
				CAAGATCTTTAATGTTGCCATTCCCCGATTCC		
				ATATGGCATGTCCAACATTCAGGGTGTCTATA		
				GCCCGATTGGTAAGTTAA		
Shigella	-	prey5237	19	GCAGCAACAGCAGCCGCCACCACCGCC	220	QQQQQPPPPIPANGQQASS
ospB	:	,		AATACCTGCAAATGGGCAACAGGCCAGCAGC		QNEGLTIDLKNFRKPGEKTFT

QRSRLFVGNLPPDITEEEMRK LFEKYGKAGEVFIHKDKGFGFI	RLETRTLAEIAKVELDNMPLRG	KOLRVRFACHSASLTVRNLPO	YVSNELLEEAFSVFGQVERAV	VIVDDRGRPSGKGIVEFSGKP	AARKALDRCSEGSFLLTIFPR	PVTVEPMDQLDDEEGLPEKLV	IKNOOFHKEREOPPRFAOPGS	FEYEYAMRWKALIEMEKOOO	DQVDRNIKE														GDFCIRVFSEKKADYGAVDUE	EANLEEFUISEDUIDUGVRNL	FACILAGEDAEISAFELUTICRE	VLAKRODIKSDGFSIETCKIMV	DMLDSDGSGKLGLKEFYILWI	KIQKYQKIYREIDVDRSG1MNS	YEMRKALEEAGFKMPCULHU	VIVARFADDQLIIDFDNFVRCL	VRLETLFKIFKQLDPENIGIIEL	DLISWLCFSVL
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CAAAATGAAGGCTTGACTATTGACCTGAAGA	CCAACGAAGCCGTCTTTTGTGGGAAATCTT	CCTCCCGACATCACTGAGGAAGAAATGAGGA	AACTATTTGAGAAATATGGAAAGGCAGGCGA	AGTCTTCATTCATAAGGATAAAGGATTTGGCT	TTATCCGCTTGGAAACCCGAACCCTAGCGGA	GATTGCCAAAGTGGAGCTGGACAATATGCCA	CTCCGTGGAAAGCAGCTGCGTGTGCGCTTTG	CCTGCCATAGTGCATCCCTTACAGTTCGAAA	CCTTCCTCAGTATGTGTCCAACGAACTGCTG	GAAGAAGCCTTTTCTGTGTTTGGCCAGGTAG	AGAGGGCTGTAGTCATTGTGGATGATCGAGG	AAGGCCCTCAGGAAAAGGCATTGTTGAGTTC	TCAGGGAAGCCAGCTGCTCGGAAAGCTCTG	GACAGATGCAGTGAAGGCTCCTTCCTGCTAA	CCACATTTCCTCGTCCTGTGACTGTGGAGCC	CATGGACCAGTTAGATGATGAAGAGGGGACTT	CCAGAGAAGCTGGTTATAAAAAACCAGCAAT	TTCACAAGGAACGAGAGCAGCCACCCAGATT	TGCACAGCCTGGCTCCTTTGAGTATGAATAT	GCCATGCGCTGGAAGGCACTCATTGAGATGG	AGAAGCAGCAGCAGGACCAAGTGGACCGCA	ACATCAAGGAGGC	TGGGGATTTCTGCATCCGGGTCTTTTCTGAA	AAGAAAGCTGACTACCAAGCTGTCGATGATG	AAATCGAGGCCAATCTTGAAGAGTTCGACAT	CAGCGAGGATGACATTGATGATGGAGTCAGG	AGACTETTTGCCCAGTTGGCAGGAGGATG	CGGAGATCTCTGCCTTTGAGCTGCAGACCAT	cctgagaagggttctagcaaagcgccaagat	ATCAAGTCAGATGGCTTCAGCATCGAGACAT	GCAAAATTATGGTTGACATGCTAGATTCGGA	CGGGAGTGGCAAGCTGGGGGCTGAAGGATT
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				AAAAATTTACCGAGAAATCGACGTTGACAGGGGGGGGGG	
Shigella ospB		prey34730	23	ATGGTGAATCCGGGCAGCTCGCAGCCG CCCCCGGTGACGCCGCTCCTCTGG AAGCGGTGCGCGCTCCTCTCTGG AAGCGGTGCCCAGGCGGGGGCAAGATT GCGGACCGCTTTCTGCTCTATGCCATGGACA GCTATTGGCAGCCGGTGCCTCAAGTGCTC CTGCTGCCAGCCGGTGCCTCAAGTGCTC CTTTGCAGAAATGACTACATTAGGTTATTTGG AAATAGCGGTGCTTGCAAAAGTGCTC CTTTGCAGAAATGACTACATTAGGTTATTTGG AAATAGCGGTGCTTGCAGCGCTTGCGGCAGC TCGATTCCTGCCAGTGAACTCGTCATCAGGG CGCAAGGCAATGTGAATCACTTAAGTGTTTT ACATGCTCTACCTGCCGGAATCGCTGGTCC CGGGAGATCGGTTTCACTACATGAGGCCAG TTTATTTTGTGAACATGAATTCACTTCAGAGC TCATCAATGGCCATTTGAATTCACTTCAGAGC	MVNPGSSSQPPPVTAGSLSW KRCAGCGGKIADRFLLYAMDS YWHSRCLKCSCCQAQLGDIG TSCYTKSGMILCRNDYIRLFGN SGACSACGQSIPASELVMRAQ GNVYHLKCFTCSTCRNRLVPG DRFHYINGSLFCEHDRPTALIN GHLNSLQSNP
Shigella ospB	4	prey33141	22	CCTGAGCCTGCCGGGGATCCTGCACTTTATC CAGCACGAGTGGGCGCGCTTCGAAGCCGAG AAAGCCCGCTGGGAGGCCGAGCCGA	LSLPGILHFIQHEWARFEAEKA RWEAERAELQAQVAFLQGER KGQENLKTDLVRRIKMLEYAL KQERAKYHKLKFGTDLNQGE KKADVSEQVSNGPVESVTLEN SPLVWKEGRQLLRQYLE

	MAASLRLLGAASGLRYWSRR	LRPAAGSFAAVCSRSVASKTP	VGFIGLGNMGNPMAKNLMKH	GYPLIIYDVFPDACKEFQDAGE	QVVSSPADVAEKADRIITMLPT	SINAIEAYSGANGILKKVKKGS	LLIDSSTIDPAVSKELAKEVEK	MGAVFMDAPVSGGVGAARSG	NLTFMVGGVEDEFAAAQELLG	CMGSNVYYCGAVGTGQAAKI	CNNMLLAISMIGTAEAMNLGIR	LGLDPKLLAKILNMSSGRCWS	SDTYNPVPGVMDGVPSANNY	QGGFGTTLMAKDLGLAQDSA	TSTKSPILLGSLAHQIYRMMCA	KGYSKKDFSSVFQFLREEETF	*															
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GAGAACAGCCCGTTGGTGTGGAAGGAGGGG	ATCCCACCTCTTACGGCTCTCGGAGCTG	AIGGCAGCCICCIIACCCCICCIICCICCICCICCICCICCICCICC	CC CCGG C CCGG AC GCAGCGCGGG	TeresticiaegicaetegecticaAagaCTCC	AGTTGGATTCATTGGACTGGGCAACATGGGG	AATCCAATGCCAAAAATCTCATGAAACATGG	CTATCCACTTATTATTATGATGTGTCCCTG	ATECCTSCAAAGAGTTTCAAGATGCAGGTGA	ACAGGTAGTATCTTCCCCAGCAGATGTTGCT	GAAAAAGCTGACAGAATTATACAATGCTGCC	CACCAGTATCAATGCAATAGAAGCTTATTCCG	GAGCAAATGGGATTCTAAAAAAAGTGAAGAA	GACCACTCATTATTATAGATTCCAGCACTATTG	ATCCTGCAGTTTCAAAAGAATTGGCCAAAGAA	CTCACACATGGGAGCAGTTTCATGGATG	CCCTRTTCTGTGTGTAGGAGCTGCACG	ATCTGGGAACCTCACGTTTATGGTGGGAGGA	GTTGAAGATGAATTTGCTGCTGCCCAAGAGT	TGCTGGGGTGCATGGGCTCCAACGTGGTGT	ACTGTGGAGCTGTTGGGACTGGGCAGGCGG	CAAAGATCTGCAACAACATGCTGTTAGCTATT	AGTATGATTGGAACTGCTGAAGCTATGAATCT	TGGAATCAGGTTAGGGCTTGACCCAAAACTA	CTGGCTAAAATCCTAAATATGAGCTCAGGAC	GGTGTTGGTCAAGTGACACTTATAATCCTGTA	ccregaergarggargccarcccrcggcra	ATAACTATCAGGGTGGATTTGGAACAACACT	CATGGCTAAGGATCTGGGATTGGCACAAGAC	TCTGCTACCAGCACAAAGAGCCCAATCCTTC	TTGGCAGTCTGGCCCATCAGATCTACAGGAT	GATGTGCAAAGGCTACTCAAAGAAGAC	TTCTCATCCGTGTTCCAGTTCCTACGAGAGG
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ATGGCAGCGTTGT GATTCTGAGAGA GGATGTTCCACA STATCATGAACTG SCCAGAGCCTTTGG SCCAGAGCAGTG TAACGATCAGGT CTGGACCAAACA AGTTAAAAAACTCT	SATCCCCCCATCC SATCCCCCCATCC TGCCAGCAGAAC TGCCAGCAGAAC TGCCAGCAGCATCG TGCAGCAGCATCG TGCCTGAGCT ACTGCCTGAGCT ACAACTGGGCC ACTATCTCAGGCT ACAACTGGCC ACTATCTCAGGCT ACAACTGGCATCGT ACAACTGGCATCTGT ACAACTGGCATCCTGT ACAACTGGCATCTGT ACAACTGGCATCCTGT ACAACTGGCATCCTGT ACAACTGGCATCCTGT ACAACTGGCATCCTGT ACAACTGGCATCCTGT ACAACTGGCATCCTGAA ACCTCCTCATCAA ACCTCATCAA ACCTCCTCATCAA ACCTCCTCATCAAA ACCTCCTCATCAAA ACCTCCTCATCAAA ACCTCCTCATCAAA ACCTCCTCATCAAAA ACCTCCTCATCAAA ACCTCCTCATCAAA ACCTCCTCAAAAA ACCTCCTCAAAAAAAA	STCTGAACCTTCC 228 LKTAGKSEPSSKLRKQLKKQQ STTAAAAAGCAGC SGACTCTTCGGT AACACGGCATCAT ATTTCAGATTTAT SAGCTGCCTCAG TVDPDCTSNQQ TVDPDCTSNQQ AAAGAATGTGAAA
CCATCAGTTTCCAAACTTAATGGCAGCGTTGT TACTGATGGTGAACGAAGATTCTGAGAGA TTTTTTATTCGTTACTATGTGGATGTTCCACA GGAAGAAGTGCCATTCAGGTATCATGAACTG GGAAGAAGTGCCATTCAGGTATCATGAACTG ATCACTAAATATGGGAAGTTGGAGCCTTTGG CAAAGTGGACCTAAGAACTTTAACGATCAGGT GGAAGAAGTAGACATTTAACGATCAGGT GGAAGAAATACG	AGTGGATGAGGTGCTGCAGATCCCCCCATCC CTGCTGACATGCGGCGCTGCCAGCAGAAC ATCGGGGACCGCTACTTCCTGAAGGCCATCG ACCAGTACTGGCAGGAGCTGCCTGAGGT GCGACCTCTGTGGCTGCCGGCTGGGTGAGG TGGGCCGCCTCTACTACAAACTGGGCC GGAAGCTCTGCGGGGGGCTGCCGGTGAGG TTTGGGCAAGACGGTCTCTGCGCCTGT TTTGGGCAAGACGGCTTCTGAGATCACAA TGCGGGTGAAGACAAGTGTATCACCTGGA ATGTTTCAAGTGCGCCCTGTCAGAAGCAT TTCTGTGTAGGTGACAAGGGATCAAAGACAACTGGAATCACTCATCAAGATGGGAATCACTCATCAAGGACAATGGGAATGAAT	CCTGAAGACAGCTGGCAAGTCTGAACCTTCC AGCAAGTTGCGAAAGCAACTTAAAAAAGCAGC AAGACTCTTTAGATGTCGTGGACTCTTCGGT CTCCTCTTTATGTCTGTCTAACACGGCATCAT CTCATGGGACCAGAAACTATTTCAGATTTAT CCAAATCTCCATTCTACCGAGCTCCTCAG GTATGAGGCCCTGGGAATGGAGGACCATT GGGCCAGACCAAATTCCTGGAAGACAAGCCT CAGTTCATCAGCAGAAATTAAAAGAATGTGAAA
	56	27
	prey12713	prey67836
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	Shigella ospB	Shigella ospB

				AGGGGACAGTCATGTCTGGCCGCAGAAAAAC TGTGGACCCAGACTGCACCTCCAACCAACAG C		
Shigella ospB	~	prey700	58	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGA ACATGAATAGACTACCAGGTTGGGATAAGCA TTCATATGGTTACCATGGGGATGATGGGACATT CGTTTTGTTCTTCTGGAACTGGACACCTTAT GGACCAACTTTCACTGGTGATGTCATTG GCTTTGTTCATTCATTATCACTGGTGATTTGGTAT TGCTTTCACTGACCTACCGCCAAATTTGTAT TGCTTTCACTGACCTACCGCCAAATTGTAT TGCTTTCACTGACTTCAACACACTCCTTTC GTGTTTGATATAGAACTATATGCGGAGATGG TTTCATTGGAAATTCCAAAAATGGTTTCATTAGTCCAAAAATGGTTTCATTAGTCCAAAAAATGGTTTCATCATCGGAGATGGTTTCATTGCAAAAAATGGTTTCATCATTGCAAAAAATGGTTTCATCATCAGACCAGACCGGCACAGACCGGCCATTGAAAAAATGGTTTCATCATCAGAAAAAATGGTTTAAGTCCACCATGGAAAAAAGGAAATAGGAAAAAGGAAACAACAACAACAACAAGAAGAACCAAGAACAAAAGGAAACAAAAGGAAACAAAAGGAAACAAAAAGGAAACAAC	229	MGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQ PYGPTFTTGDVIGCCVNLINNT CFYTKNGHSLGIAFTDLPPNLY PTVGLQTPGEVVDANFGQHP FVFDIEDYMREWRTKIQAQID RFPIGDREGEWQTMIQKMVS SYLVHHGYCATAEAFARSTDQ TVLEELASIKNRQRIQKLVLAG RMGEAIETTQQLYPSLLE
Shigella ospB	-	prey67844	59	TTCCATACAGGAACCCCATCTGAAGGTCACC AACATCAAAGACCAAAGGTAGATAAATCCAC GAAGTTGAGGAAAAACCAGTGCAAAAAGGCT GAGAATTCCAAAAACCAGAAAGGCTCTTCTC CTCCAAAGGATCAAAACTCCTCGCCAGCAAG GGAACAAACCCAGAAAGGCTTTGTC TCCAAAGGATCAAAACTCCTCGCCAGCAAG GAACAAAACTCAGAAAGGTTGAT GAATAACAAAGTAAGGATTAAAGAACTTGAA ACCAATGCAAGGAAGTTAAAGAACCTTGAAA	230	FHTGTPSEGHQHQRPKVDKS TKLRKNQCKKAENSKNQKGS SPPKDQNSSPAREQNQMENE FDELTEVGFRRWVITSKLKEH VLTQCKEVKNLEKRL
Shigella ospB	-	prey67853	တ္တ	GCCGTGGACGGTGAGGGTGCCGGCCTCACC TCGGAGGCATGGAAGTACCAGGTTACTTCAC	231	AVDGEGAGLTSEAWKYQVTS HREDRFPLSSRLRLALKNLGA

	ATCGAGAGGACCGITTICCTCTTTCAGTCG GCTGCGGTTGGCACTGAGGATCTTGGTGCT GACAGACACAGAGCAGGGTCTCTCGTGGAA CAGGAGTTGTCTGGTCGTTTCAGTTTGATGA GTGGCAGAAAATGAGACGATGGGAAGTGTGT GTGTGGCCTNTTTTNGGTGCTNNGGNNGN NN	GRK*DDGKCVCGPXFXCXGX
 prey66272 31	ATGTGGGCCCTGGGTCAAGCAGGTTTTGCCA 232 ACCTCACCGAGGGACTGAAAGTGTGGCTGG GGATCATGCTGCCTGTGCTGGGCATCAAGTC TCTGTCTCCCTTTGCCATCACACCTGCATC GGCTGCTCCCTTTGCCATCCCAACGTTC TCCCACTTCGGCATCACCCCAAGGACTTC TCCCACTTCTGGACTTTGCCAACGACTTC TCCCACTTCTGGACTTTGCCTATTGCCGAA GGCTTCGGCATCTACCCCCAGCGCAC GCTGTCACCTCTACCCCCAGCACCTCAAGA CAACTCCCTGACACCTCTTTCCAGAAGTG CTGCATTTGGAGCTCTTCCTTTTCCTGTCCAGA GCTGTGTCAGCTCTTCCTTTTCCTGTCCAGA GCTGTGCAACAAGCAGCTCTGACCTGAGAAGT AAGAGCTCTGAGCACCTGACTGAGAAGA AAGAGCTCTGAGCACCTGTCAGAG GCCACCCCTAGCTGCCCCAAGAAGGAA AAGAGCTCTGGAGACCATTCAGGCCT CCTGGGAGCAGCTGTGCTGCAGAAG GTCTTTGCAAGAAACCATTCAGTCCCTCAAG GTCTTTGCAAGAACCATTCAGTCCTCAAG GTCTTTGCAAGAACCATTCAGTCCTCAAG CTTACCAACCAGGAGCTGCTGTGA CATGGCCTGCAGGATGTCGTCACCTGTGA CATGGCCTGCAGGATGTCGTCACCTGTGA CATGGCCTGCAGGATTTGCAGCACCTGTGA CATGGCCTGCAGGATTTCCCTGTGACCTCTCTGTGA CATGGCCTGCTGCTGTGACCTGTGA CTCCTGTTGCCTGCTGCTCTCTGTGA CTCCTGTTGCCTGCTTTGCTGCTCTTGCTC CTCCTGTGCCTTCTTTACCAGCTC CTTCCAGGCTCCTTTGCTGCTCTTTGCTTCCTCTTTCCAGGCTTCCTTTTCCAGGCTTCTTTCT	MWALGQAGFANI TEGLKYWL GIMLPVLGIKSLSPFAITYLDRL LLLMHPNLTKGFGMIGPKDFFP LLDFAYMPNNSLTPSLQEQLC QLYPRLKVLAFGAKPDSTLHT YFPSFLSRATPSCPPEMKKEL LSSLTECLTVDPLSASVWRQL YPKHLSQSSLLLEHLLSSWEQI PKKVQKSLQETIQSLKLTNQEL LRGSSNNQDVYTCDMACKG LLQQVGGPRLPWTRLLLLLLV FAVGFLCHDLRSHSSFQASLT GRLLRSSGFLPASQQACAKLY SYSLQGYSWLGETLPLWGSH LLTVVRPSLQLAWAHTNATVS FLSAHCASHLAWFGDSLTSLS QRLQIQLPDSVNQLLRYLREL PLLFHQNVLLPLWHLLEALA WAQEHCHEACRGEVTWDCM KTQLSEAVHWTWLCLQDITVA FLDWALALISQQ*

Shigella ospD1	2 2	prey700	33	000	233	MGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQ PYGPTFTTGDVIGCCVNLINNT CFYTKNGHSLGIAFTDLPPNLY PYGLQTPGEVVDANFGQHP FVFDIEDYMREWRTKIQAQID RFPIGDREGEWQTMIQKMVS SYLVHHGYCATAE TNLKRQANKKSEGSLAYVKG GLSTFFEAQDALSAIHQKLEAD
				GGICICAGIACATICITCGAAGCACAGGATG CCCTCTCAGCCATCCATCAAAAACTAGAAGC		GTEKVEGSMTQKLENVLNRA SNTADTLFQEVLGRKDKADST

	<u> </u>	ACGCAGAAACTGGAGAATGTTCTGAACAGAG	NIQKGDYDVVINDYEKAKSLF
	<u></u>	CAAGTAATACTGCAGACACATTGTTTCAAGAA	GKTEVQVFKKYYAEVETRIEAL
	<u>-</u>	GTATTAGGTCGGAAAGACAAGGCAGATTCCA	RELLLDKLLETPSTLHDQKRYI
		CTAGAAATGCACTCAATGTGCTTCAGCGATTT	RYLSDLHASGDPAWQCIGAQ
	4	AAGTTTCTTTCAACCTTCCTCTAAATATTGAA	HKWILQLMHSCKEGYVKDLKG
	4	AGGAATATTCAAAAGGGTGATTATGATGTGGT	NPGLHSPMLDLDNDTRPSVLG
		TATTAATGATTATGAAAAGGCCAAGTCACTTT	HLSQTASLKRGSSFQSGRDD
		TTGGGAAAACGGAGGTGCAAGTTTTCAAGAA	TWRYKTPHRVAFVEKLTKLVL
	<u> </u>	ATATTATGCTGAAGTAGAAACAAGGATTGAAG	SQLPNFWKLWISYVNGSLFSE
		CTTTAAGAGAATTACTTCTGGATAAATTGCTT	TAEKSGQIERSKNVRQRQNDF
		GAGACACCATCAACTTTACATGACCAAAAAC	KKMIQEVMHSLVKLTRGALHP
		GTTACATAAGGTACCTGTCTGACCTTCATGC	LSIRDGEAKQYGGWEVKCELS
	<u></u>	GTCTGGTGACCCTGCTTGGCATTGGA	GQWLAHAIQTVRLTHESLTAL
	<u></u>	GCCCAACACAGTGGATCCTTCAGCTCATGC	EIPNDLLQTIQDLILDLRVRCV
	∀	ACAGTTGCAAAGAGGCTACGTGAAAGATCT	MATLQHTAEEIKRLAEKEDWIV
	<u></u>	GAAAGGTAACCCAGGCCTGCACAGTCCCATG	DNEGLTSLPCQFEQCIVCSLQ
		TTGGATCTTGATAATGATACACGTCCCTCAGT	SLKGVLECKPGEASVFQQPKT
		GTTGGGCCATCTCAGTCAGACAGCGTCCCTG	QEEVCQLSINIMQVFIYCLEQL
	▼	AAGAGGGCAGCATTTCAGTCTGGTCGA	STKPDADIDTTHLSVDVSSPDL
	<u></u>	GACGACACGTGGAGATACAAAACTCCCCACA	FGSIHEDFSLTSEQR
	<u></u>	GGGTGGCCTTTGTTGAAAATTGACAAAACT	
		CGTCTTGAGCCAGCTGCCTAACTTCTGGAAA	
		CTCTGGATCTCCTACGTTAATGGAAGCCTCTT	
		CAGTGAGACTGCTGAGAAGTCAGGCCAGATT	
	<u> </u>	GAAAGATCAAAGAATGTAAGGCAAAGACAAA	
	<u> </u>	ATGATTTTAAGAAAATGATTCAGGAAGTAATG	
		CACTCCCTGGTGAAGCTTACCCGCGGAGCC	
		CTGCATCCCCTCAGCATCCGGGATGGGGGAA	
	<u></u>	GCCAAGCAGTACGGAGGCTGGGAGGTGAAG	
	 	TGCGAGCTCTCCGGACAGTGGCTCGCTCAC	
	<u>-</u>	GCCATCCAGACTGAAGACTTACTCATGAATC	
	<u></u>	GTTGACTGCCCTTGAAATTCCTAATGACCTGT	
_	_	TACAGACTATCCAGGATCTCATCTTGGATCTC	
		CGAGTACGTTGCGTAATGGCCACGTTGCAGC	
	<u> </u>	ACACGGCGGAAGAATAAAGAGATTAGCTGA	
	<u> </u>	AAAAGAAGACTGGATTGTTGACAATGAAGGA	

				CTGACTTCTCTACCATGTCAGTTTGAACAGTG CATCGTGTGTTCTCTGCAGTCACTGAAGGGG GTTCTGGAGTGCAAGCCGGGAGAGGCTAGT GTCTTCCAACACCTAAAACACAGGAGGGGG TTTGCCAACAACCTAAAACACAGGAGGTTTTGCCAGCTAAGCATCAATATAATGCAGGTT TTATATACTGTCTGGAACAGTTGAGCACCAA GCCTGATGCAGATATAGATACACATCTCT CTGTTGATGTTTCTTCCCCTGACTTGTTTGGA AGTATCCATGAAGACTTCAGCTTGACCTCAG		
Shigella ospD1	8	prey67651	34	CAGTATAAGAAGGCCTTAGAGAATGAAACAA ATGAGGAGAAATCTGGCACACCAGGAGCTGA TAAAGCAGAAAAAAGATATAAGTATACAGTTA AGCTCANCCCAGTCTCGTTGTACTCTTCTAGA GAACCAACTAGAATATACAAAGAGAATGTT CTCAACGTAGGAGCGAGAAAAGAGAAAAGAAA	235	QYKKALENETNEEKSGTPGAD KAEKRYKYTVKLXPVSLYSSR EATRIYKENGSQRRSEKRT*S* NNRPSFRGKKNKIR*SCMQNL KSLMSXKKSVSDLQQLX
Shigella ospD1	8	prey67653	35	CCCTGAAATCTGCAAAATGGCTGATAATTTGG ATGAATTTATTGAAGAGCAAAAAGCCAGATTG GCCGAAGACAAAGCAGAGGTTGGAAAGTGATC CACCTTACATGGAAATGAAGGGAAAGTTGTC AGCGAAGCTTTCTGAAAACAGTAACGG ATCTCTATGGCTAAGGAAAACATACCACCAAA TAGTCAACAGACCAGGGGTTCCTTAGGAATT GATTAGGATTAAGTTTACCACTTGGAGAAGA CTATGAACGGAAGAACATAAAATTAAAAAGAAG	236	PEICKMADNLDEFIEEGKARLA EDKAELESDPPYMEMKGKLS AKLSENSKILISMAKENIPPNS QQTRGSLGIDYGLSLPLGEDY ERKKHKLKEEL
Shigella ospD1	2	prey67667	96	CGACCAGGGCACCCCAGTACATGGAGAA CATGGAGCAGGTGTTTGAGCAGTGCCAGCA GTTCGAGGAAACGCCTTCGCTTCTTCCGG GAGGTTCTGCTGGGGTTCAGAAGCCCTAA ACCTGTCCAATGTGGCTGGTTACAAAGCCAT	237	DQGTPQYMENMEQVFEQCQ QFEEKRLRFFREVLLEVQKHL NLSNVAGYKAIYHDLEQSIRAA DAVEDLRWFRANHGPGMAM NWPQFEEWSADLIRTLSRREK

TTACCATGACCTGGAGCATCAGAGCA GCTGATGCAGTGGAGGTGGTTC GCTGATGCAGTGGAGGACCTGAGGTGGTTC CGAGCCAATCACGGGCATGGCCATG ACTGGCCGCAGTTTGAGGAGTGGTCCGCA GACCTGATTCGAGGAGTGGTCCGCA AGAAGAAGGCCACTGACCCTGAC GGGCATCAACCAGCAGAGAGA CCGAGTAAGCCCAGCACAGTTTTTG CCGAGTAAGCCCAGCACAGCA	### STATEMENT NOT CONTROLLED NOT CON	67501 38 CTTCCGCCTGGAACAGCTGGAATGCCTTGAT 239 FRLEQLECLDDAEKKLNLAQK GATGCAAAAAAATTAAAAATTGGCCCAGA AATGCTTTAAAAAATTGTTACGGAGAAAATCAT CAGAGACTGGTCCACATAAAAGGAAATTGTG GAAAAGGAAATTCTAAAAAGGAAATTGTAAAAAGGAAATTGTAAAAAGGAAATTGTAAAAAGGAAATTGTAAAAATTGTAAAAATTGTAAAAATTGTAAAAATTGTAAAAATTGTAAAAAA
	prey67657	prey67501
		2
	Shigella ospD1	Shigella ospD1

			GGAAATGATGTAGAGGCTTATGAGTATCTTAA GGAAATGATGTAGAGGCTTATAAA CAGGCACGTCAGCTCTTTAAAGAGCTATATAT TGATCCATCAAAGTGGACAATTTGTTGCAGT TGGGTTTACTGCCCAGGAAGCACGTGGGCTTG GCCTGAGGCCGTGTGATGGGAACGTGGATC ATGCGGCCACTCATATTACCAACCGCAGAGA GGAACTGGCCCAAATAAGGAAGGAGGAAGAA GAGAAGAAAAGGCCCCCCCAGGAAAA GAGAAGAAAAGGGATGGGCTACTCCACGCA		ELAQIRKEEKEKKRRLENIRF LKGMGYSTH
Shigella 2	prey67678	6E	GACCAGCTGAGGGTGTTGGACCCAGAGGTT GCACAGCAGACCATAGAGCTGAAGGAAGAGT ACCCAGCAGACCATAGAGCTGAAGGAAGAGT GCAAAGACTTTGTGGACAAAATTGGCCAGTT TCAGAAATTGTGGTGGTTTAATTGACCAGTT TCAGAAATGGCAAAAGCAGAAAATGAA AAGATGAAGCCATCGGTGCTCGGAACTTGC TCAAATCTATAGCAAAGCAGAGAAGCAGAA ACAGCAGCAACTTCAAGCCCTAATAGCAGAA AAGAAATGCAGCTTGTGTAAAGTAGCAGAA CAAAATGCAGCTTGTGTAAAGTAGCAGAA CAAAATGAAGTTTGTGTAAAGTAGAAGCAGAA AAATGA	0;	NKLRVLDPEVTQQTIELKEECK DFVDKIGQFQKIVGGLIELVDQ LAKEAENEKMKAIGARNLLKSI AKQREAQQQLQALIAEKKM QLERYRVEYEALCKVEAEQNE FIDQFIFQK*
Shigella 2 ospD1	prey67578	04	ATGGCGGTGGAGACTCTGTCCCCGGACTGG GAGTTTGACCGCGTTGACGACGCTCGCAG AAAATTCATGCCGAAGTCCAACTTAAGAATTA TGGGAAATTCTTGAGGAGTATACCTCTCAAC TGAGAAGATTCTTGAGGAGTATACCTCTCAAC TGAGAAGATTGTTGGGATTTCAATCTTGATC CATAGCATTAAAGCTTTTGCCTTATGAACAG CCTCTCTTTTGGAACTCATCAAAAA CCAGGTCTTAAACAAACTCATAAAAA CCAGGTCTTAAACAAATTTACAATGGTCT CTGCACTTTGTGGAAATTTACAATGGTCT CTGCACTTTGTGGAAATTTACAATGGTCT CTGCATTTATGGAGAAGTCACAGATTCAAA AGCATGGTGGAAAGGAGTCAAATTCAAA		MAVETLSPDWEFDRVDDGSQ KIHAEVQLKNYGKFLEEYTSQL RRIEDALDDSIGDVWDFNLDPI ALKLLPYEQSSLLELIKTENKVL NKVITVYAALCCEIKKLKYEAE TKFYNGLLFYGEGATDASMVE GDCQIQMGRFISFLQELSCFV TRCYEVVMNVVHQLAALYISN KIAPKIIETTGVHFQTMYEHLG ELLTVLLTLDEIIDNHITLKDHW TMYKRLLKSVHHNPSKFGIQE EKLKPFEKFLKLEGQLLDGMI

				TCCCAACACCCCGCTGCTC AGGATGAACCTGGAGGCCCACCTCCAAGGAG TGCGAGCACATCAAATGCCCCCCACTCCAAGT TGCGAGCACATCAAATGCCCCCCACTCCAAGT ACGGGTGCACGTTCATCGGGAACCAGGAC CTTACGAGACCTGGAGACTTGCCGCTT CGAGGCCTGAAGGAGTTTCTGCAGCAGAC GGATGACCCTTCCACGAGATTCTGCAGCGTC CTGGCCCAGAAGGACTTCCACGAGATCGCCTTC CTGGCCCAGAAGGACCAGGAGATCGCCTTC CTGCCCCAGAAGGACCAGGAGATCGCCTC CTGCGCTCCATGCTGGGAAAGCTCTCGGAGA		
Shigella ospD1	2	prey3160	42	ACATGAACTTACGGTTATGCAAG AACAAGCAAGACAAGA	243	RKLHELTVMQDRREQARQDL KGLEETVAKELQTLHNLRKLF VQDL
Shigella ospD1	7	prey50427	£43	ATGGAGGAGTATGAGAAGTTCTGTGAAAAAA ATGGAGGAGTTCTGAGGAGTCTGAG GTCTTGCCAGAATACAAGAAGCATCACTATC CACAGAGAGCTTTCTCCCTGCTCAGTCTGAA AGTATCTCACTTATTCGCTTTCATGGAGTGGC TATCCTTTCTCCACTGCTTAACAAAAGCAAAGC	244	MEEYEKFCEKSLARIQEASLS TESFLPAQSESISLIRFHGVAIL SPLLNIEKRKEMQQEKQKALD VEARKQVNRKKALLTRVQEIL DNVQVRKAPNASDFDQWEME TVYSNSEVRNLNVPATFPNSF PSHTEHSTAAKLDKIAGILPLD NEDQCKTDGIDLARDSEGFNS PKQCDSSNISHVENEAFPKTS SATPQETLISDGPFSVNEQQD LPLLAEVIPDPYVMSLQNLMKK SKEYIEREQSRRSLRGSMNRI VNESHLDKEHDAVEVADCVKE KGQLTGKHCVSVIPDKPSLNK SNVLLQGASTQASSMSMPVL ASFSKVDIPITTGNSPPVLESNS DFKVIPTIVTENNVIKSLTGSYA KLPSPEPSMSPKMHRRR

	DSPTSGRPGVTSLTTAAAFKP VGSTGVIKSPSWQRPNQGVP STGRISNSATYSGSVAPANSA LGQTQPSDQDTLVQRAEHIPA GKRTPMCAHCNQVIRGPFLVA LGKSWHPEEFNCAHCKNTMA YIGFVEEKGALYCELCYEKFFA PECGRCQRKILGEVINALKQT WHVSCFVCVACGKPIRNNVF HLEDGEPYCETDYYALFGTIC HGCEFPIEAGDMFLEALGYTW HDTCFVCSVCCESLEGQTFFS KKDKPLCKKHAHSVNF*
	245
ACAGGATCTACCACTTTTGGCAGAGGTCATC CCAGATCCCTATGTAATGAGTCTTCAGAATCT GATGAAAAGGCAATATATAGAAAGA GAACAATCTAGACGCAGTCTGAGAAGA GAACAATGTAATGAGAGTCTTAGAC AAGAACATGATGTTAATGAGAGTCATTTAGAC AAAGAACATGATGTTAATGAGAGTGCTGACT GTGTAAAAGGAAAGG	GGACAGCCCAACCTCTGGCAGACCAGGGGT TACCAGCCTCACAACTGCAGCTGCCTTCAAG CCTGTAGGATCCACTGCCGTCCATCAAGCCCCCCCCCTCCAGGCCCAAGCCAAGCCAAGCCAGGCTAC CTTCCACTGGAAGAATCTCAAACCAAGCAGTAC CTTCCACTGGAACAACCCAGCCCAACTCA GCTTTGGGACAACCCAGCCCAAGTGC ACACTTTGGGACAACCCAGCCCAAGCACTCC ACACTTTGGGACAACCCAGCCCAAGCAGC ACACTTTGGGACAACCCAGCCCAAGCAACCATTCTAGCCAGGGCAAACCCAAGGGCCCCATTCTAGCCCCCATTCTAGCCCCCTTTGGAAACTTGGAAAATCTTTGCCCTTGGAAAATCTTTGCCCTTGGAAAGGCCCAAAGGAAACCTTGGGAAAGCCAAAGGCAAAGCCAAATGTTGCCAAAAGCCAAAGGTTTGGAAAAGCCCATTCGGAACAATGTTAGCCCTTGGAAAGCCCATTCGGAACAATGTTAGCCCTTGGAAAGCCCATTCGGAACAATGTTAGCCCTTGGAAAAGCCCATTCGGAACAATGTTACCTTGGAAAAGCCCATTCGGAACAATGTTACCTTGGAAAAGCCCATTCGGAACAATGTT
40007404000047400	44
	prey63765
	8
	Shigella ospD1

				TTTCACTTGGAGGATGGTGAACCCTACTGTG AGACTGATTATTATGCCCTCTTTGGTACTATA TGCCATGGATGTGAATTTCCCATAGAAGCTG GTGACATGTTCCTGGAAGCTCTGGGCTACAC CTGGCATGACACTTGCTTTGTATGCTCAGTGT GTTGTGAAAGTTTGGAAGGTCAGACCTTTTC TCCAAGAAGGACAAGCCCCTGTGTAAGAAAC		
Shigella ospD1	2	prey67623	45	ACATGGTAC GATGACAA GGATAGTGAT ACCACTGAAT ACCATTCA ACCATTACTT GTGACCGAC GAAAGAGTC ACCATTACCAT ACTTTACCAT ACTTTACCAT ACTTTACCAT CCGAGAAG CTTTACCAT ACTTTACCAT ACTTTACCAT ACTTTACCAT ACTTTACCAT CCGAGAAG CTCAACTAC ACCAATGC ACCAATGC ACCAATGC ACCAATGC ACCAATGC ACCCAATGC ACCTAACTACAA AACTTACAA AACTTACAA AACTTACAA AACTTACAA ACCAATGC ACCAACTC ACCAACT ACCAACTC ACC	246	FYRRHTPYMVQPEYRIYEMNK RLQSRTEDSDNLWWDAFATE FFEDDATLTLSFCLEDGPKRY TIGRTLIPRYFSTVFEGGVTDL YYILKHSKESYHNSSITVDCDQ CTMVTQHGKPMFTKVCTEGR LILEFTFDDLMRIKTWHFTIRQ YRELVPRSILAMHAQDPQVLD QLSKNITRMGLTNFTLNYLRLC VILEPMQELMSRHKTYNLSPR DCLKTCLFQKWQRMVAPPAE PTRQP
Shigella spD1	2	prey7315	46	ATGCTGGATAGGGATGTGGGCCCAACTCCCA 22 TGTATCCGCCTACATACCTGGAGCCAGGGAT TGGGAGGCACACCATATGGCAACCAAACT GACTACAGAATATTTGAGCTTAACAAACGGCT	247	MLDRDVGPTPMYPPTYLEPGI GRHTPYGNQTDYRIFELNKRL QNWTEECDNLWWDAFTTEFF EDDAMLTITFCLEDGPKRYTIG

			TCAGAACTGGACAGAGGAGTGTGACAATCTC TGGTGGGATGCATTCACGACTGAGTTCTTTG AGGATGATGCCATGTTGACCATCATTTTG CCTGGAGGATGACCAAGAGATATACCATT GCCGGACCCTGATCCCACGCTACTTCCGCA GCCGGACCCTGATCCCACGCTACTCCGCA GCATCTTTGAGGGGGGTGCTACGGAGCTTC CCAGCAACTTTGTGTCCCTCGACTGTGACC AGGCAACTTTGTGTCCCTCGACTGTGACC AGGCAACTTTGTGTCCCTCGACTGCAGC CCATGTTCACCCAGGTGTGTGTGGGGGCC GGTTGTACCCGGAGTTCATGTTTGACGACT GGTTGTACCTGGAGTTCATGTTTGACGAGC CCATGTTCACCCAGGGCTCCCCCGCAGC GGTTGTACCTGGAGTTCATCCCCCCGCAGC GGTTGTACCTGGAGTTCATCCTCCCCCAGA ATCCTTGCCATGCTCCCAAGACCCCCAGA TGTTGGATCAGCTCCCAAAAACATCCCCCCAGG GTGTGGGCTGTCCAAAAACACTAC CTCCGACTCTGTGTGATACTCCACTACG AAGAGCTCTTGTGTGATACTCCACACAGC CTCCGACTCTGTGTCACACACACACACACACACACACACA		RTLIPRYFRSIFEGGATELYYV LKHPKEAFHSNFVSLDCDGGS MYTQHGKPMFTQVCVEGRLY LEFMFDDMMRIKTWHFSIRQH RELIPRSILAMHAQDPQMLDQ LSKNITRCGLSNSTLNYLRLCV ILEPMQELMSRHKTYS
Shigella 2 ospD1	prey67601	47	C AGTCACTGCTTCAACCACCTGTGAGAATTA AGAAAAGCCAGGAATGAGTTACAAACAGTT ATGAAGCATTCGTCCAGCAGCAGCTGT ATGAAGCATTCGTCCAGCAGCAGCTGA AAAAACAGAACGAGAATCGGCTTAAAGAG TTTTACACCAGGGAGTATGAAAAGCTTCGGG ACACTTACATTGAAGAAGCAGAAATTGCAATTGCAAGAAGCAGTTGAAATTGCAATTGCAAGAACCTCTAAGTTGAAATTGCAATTGCAAGAACTTCAGAAATTGCAATTAAGAAAGCCATGAAATTGCAAGAAATTGCATTAAGAAAGCCATGAAATTGAAAAATGAAAATGAAAATCAATGAAAAATCATGAAAAATTGAAAAAAAA	248	VTASTTCEKLEKARNELQTVY EAFVQQHQAEKTERENRLKEF YTREYEKLRDTYIEEAEKYKM QLQEQFDNLNAAHETSKLEIE ASHSEKLELLKKAYEASLSEIK KGHEIEKKSLEDLLSEKQESLE KQINDLKSENDALNEKLKSEE QKRRAREKANLKNPQIMYLEQ ELESLKAVLEIKNEKLHQQDIK LMKMEKLVDNNTALVDKLKRF QQENEELKARMDKHMAISRQ LSTEQAVLQESLEKESKVNKR LSMENEELLWKLHNGDLCSPK RSPTSSAIPLQSPRNSGSFPS PSISPR*

Shigella 2 ospD1	prey53735	84	TCTAGAACAGGAGTTAGAAAGCCTGAAAGCT GTGTTAGAGCTCAAGAATGAGAAACTGCATC AACAGGACATCAAGTTAATGAAAATGGAGAA ACTGGTGGACAACACACAGCATTGGTTGAC AAATTGAAGCGTTTCCAGCAGCAGTGAG AATTGAAAGCTTCCAGCAGGAGAATGAG AATTGAAAGCTTCCAGCAGGAGAATGAG AATTGAAAGCTTCCAGCAGGAGAATGAC AATCTCAAGGCATTCCACGGAGCAGCT GTTCTGCAAGGCATTCCACGGAAACGA AAGTCAACAGCACTTTCCACGGAAACGA AAGTCAAGAGCTTCTTTCAGCAAAGCAA	G	SLPPSTGTFQEAQSRLNEAAA GLNQAATELVQASRGTPQDLA RASGRFGQDFSTFLEAGVEM AGQAPSQEDRAQVVSNLKGIS MSSSKLLLAAKALSTDPAAPN LKSQLAAAARAVTDSINQLITM CTQAPGQKECDNALRELET	
			TCTCCATGTCTTCAGGCAACTTCTTCTGGCT GCCAAGGCCCTGTCCACGGACCCTGCTGCC GCCAAGGCCCTGTCCACGGACCTTCTTGGCT GCCAAGGCCCTGTCCACGGACCTTCTGGCT CCTAACCTCAAGAGTCAGCTGCTGCTGCC CCAGGGCAGTAACTGACAGCATCAGCT CAGAGGAGTGTGATAACGCCCTGGGGAAT TGGAGACGGTCCGGGAACC CAGTCCAGCCCATCAATGGACATCTT GGTTGCCTGGACAGTGTCCTACTTT GGTTGCCTGGACAGGCCATCAATGGACACC CAGTCCAAGACCCATCAATGGACACCTCAA AGGTGCTGGACAGGCCATCAATGGACATCT CCCAAAATGCCAAGAACCCTGCAAA GCTTGTGGCGAGGCCATCACAAAG		VKELLENPVQPINDMSYFGCL DSVMENSKVLGEAMTGISQNA KNGNLPEFGDAISTASKALCG FTEAAAQAAYLVGVSDPNSQA GQQGLVEPTQFARANQAIQM ACQSLGEPGCTQAQVLSAATI VAKHTSALCNSCRLASARTTN PTAKRQFVQSAKEVANSTANL VKTIKALDGAFTEENRAQCRA ATAPLLEAVDNLSAFASNPEF SSIPAQISPEGRAAMEPIVIS	

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				AGGC IGCATATOTOST TOST STOTOTOST AGGC CAATAGCCAAGGTGGACAGGGGCTAGTG GAGGGCTAGTG GAGGGCTAGTG GAGTTGCCCGTGCAAGGGGCTAGTG GAGTTTGCCCGTGCAAGGGGCTAGTG GCCTGCCTGCCCAGGTGCTTCTCTGCCCACGGTGCTTTTGTGCCATTGTGGCTAAACACCCTTGTGCCCAAGGGCCTACTGCCCAAGGGCCAACAGGCCAACAGGCCAACAGGCCAACAGCCCAAGGCCGCC		
Shigella ospD1	5	prey67630	49	GAGGACCTGCAGCCCCGGCCCTGTCG GAGGACCTGCAGCCCCCGGCCCCTGTCG GCCCCTTCACCACACAGCCCCCGCTCGCTCG CCCTGGGCGCAGCGCCTGGCTCTG CCTGGGCGCAGGGCCCTGAAGAACTCCCG TGTATCCTTTGTCTCAGAGGATGACGTCATGAACTA TCAGTACGGATTCAACGGTCATGTCAC TCAATACAAGAATCCAAGGCCT TCAATACAAGAATCTGGCAN	250	EDLQPPSALSAPFTNSLARSA RQSVLRYSTLPGRRALKNSRL VSQKDDVHVCILCLRAIMNYQ YGFNLVMSHPHAVNEIALSIN NKNPRTKALVLELLA
Shigella ospD1	2	prey12665	20	GAAGCGCACGAGTGATCAAGAACCG GAAGCGCACGAGTGCCGGAGAACCG GGAGTCAGCCTGCCAGTCCGGAGAAGAA GAAGAGTATCTGCAGGGACTGGAGAGGAC GCTGCAAGCAGTACTGGCTGACACCAGCAG GCTGCAAGCAGTACTGGCTGCCTCCGGCGG CCGCCGAGAATGCTGCCTCCGGCGG CGGCTGGAGAATGCTGCTTCCTCCGCGGG GAGCTCAAGTTAGGGTCTGGAAACAGC GAGCTCAAGTTAGGGTCTGGAAACAGG	251	KRHERMIKNRESACOSRRKK KEYLOGLEARLOAVLADNOOL RRENAALRRRLEALLAENSEL KLGSGNRKVVCIMVFLLFIAFN FGPVSISEPPSAPISPRMNKG EPQPRRHLLGFSEGEPVOGV EPLOGSSQGPKEPQPSPTDQ PSFSNLTAFPGGAKELLLRDL DOLFLSSDCRHFNRTESLRLA

	ESEVSEHLSASSASAIQQDSI SSMQPPSEAPMVNTVSSAYS EDFENSPSLTASEPTAHSKES LDRTLDALSESSSVKTDLPQ TAESRKKSGRHVTRVLVKDTA VQTPDPAFTYEWTKVASMAA MGPALGGAYVDPTPIANHVIS ADAIEALTAYSPAVLALHDVLK QQLSLTQQFIQASRHLHASLL RSLDADSFHYHTLEEAKEYIR CHRPAPLTMEDALEEVNKEL*
1000	TGAGAGCGAGGTCTCGGAGCATCTCAGTGC CAGCTCGGCTTCTGCCATCCAGCAGGACAGC CAGCTCGGCTTCTGCCATCCAGCAGGACAGC ACTTCCAGCATGCAGCCATCTGAAGCCC CCATGGTGAACACAGTCAGCTTATTC GGAGGATTTTGAAAACTCTCCAAGTCTGACA GCATCTGAGCCAACCGCCCATTCCAAGGAGT CTCTTGACAGAACACTGGACGCTTTGTCAA ATCCTCTTCAAGTGTGAAGACACTTCCA CAAACAGCCGAGTCTAGGAAAAGTCGGGCA CAAACAGCCGAGTCTAGGAAAAGTCGGGCA GGCATGGAACACTGGCAACCTTCAC TACGAGTGCAAGGGTGCTTGTGAAGGCCTAC GTGGACCCAAGAGTGCTTGTGAAGGCCTAC GTGCAGGCCCAGCTGCCAGCCTTCACC TACGAGTGCAATAGATGCAATCATGAT GTGGACCCGACACCCTGCACCCTGCAC CAGTTCATCCAGGCCAGCCTGCAC GCCTCCTGCAGCCGGCCCTGCAC GCCTCCTCCACGCCCTGGACCCCCCCTCCCTGCACCCCCCCC
	221
	prey67631
	α
	Shigella ospD1

prey20143	43	52	AGGACCTGGAGGAG TCCTGCGGCTCCTAG	253	MAESRQDLEEEYEPQFLRLLE RKEAGTKALQRTQAEIQEMKE
			AGAGGAAAGAAGCTGGGACCAAAGCTCTGCA		ALRPLOAEAROLRLONRNLED
			GAGAACCCAGGCTGAGATCCAGGAAATGAAG		QIALVROKRDEEVQQYREQLE
			GAGGCTCTGAGACCCCTGCAAGCAGAGGCC		EMEERQRQLRNGVQLQQQK
			CGGCAGCTCCGCCTGCAAACAGGAACCTG		NKEMEQLRLSLAEELSTYKAM
			GAGGACCAGATCGCACTTGTGAGGCAAAAAC		LLPKSLEGADAPTSQAGGMET
			GAGATGAAGAGGTGCAGCAGTACAGGGAAC		QSQGAV*
			AGCI GGAGGAAAI GGAAGAACGCCAGAGGC		
			AGTTAAGAAATGGGGTGCAACICCAGCAACA		
			ACTUTACTOR AGABOTICITATATAAGGC	٠	
			TATGCTACTACCCAAGAGCCTGGAACAGGCT		
			GATGCTCCCACTTCTCAGGCAGGTGGAATGG		
			AGACACAGTCTCAAGGGGCTGTTTAG		
prey	prey1418	53		254	WVIPDPEEEPERKRKKGPAPK
			GAGCGCAAGCGAAAGAAGGGCCCCAGCCCCG		MLGHELCRVCGDKASGFHYN
			AAGATGCTGGGCCACGAGCTTTGCCGTGTCT		VLSCEGCKGFFRRSVVRGGA
			GTGGGGACAAGGCCTCCGGCTTCCACTACAA		RRYACRGGGTCQMDAFMRR
			CGTGCTCAGCTGCGAAGGCTGCAAGGGCTT		KCQQCRLRKCKEAGMREQCV
			CTTCCGGCGCAGTGTGGTCCGTGGTGGGGGC		LSEEQIRKKKIRKQQQQESQS
			CAGGCGCTATGCCTGCCGGGGTGGCGGAAC		QSQSPVGPQGSSSSASGPGA
			CTGCCAGATGGACGCTTTCATGCGGCGCAAG		SPGGSEAGSQGSGEGEGVQL
			TGCCAGCAGTGCCGGCTGCGCAAGTGCAAG		TAAQELMIQQLVAAQLQCNKR
			GAGGCAGGGATGAGGGAGCAGTGCGTCCTT		SFSDQPKVTPWPLGADPQSR
			TCTGAAGAACAGATCCGGAAGAAGAAGATTC		DARQQRFAHFTELAIISVQEIV
			GGAAACAGCAGCAGGAGTCACAGTCAC		DFAKQVPGFLQLGREDQIALL
			AGTCGCAGTCACCTGTGGGGCCGCAGGGCA		KASTIEIMLLETARRYNHE
			GCAGCAGCTCAGCCTCTGGGCCTGGGGCTT		
			CCCCTGGTGGATCTGAGGCAGGCAGCCAGG		
			GCTCCGGGGAAGGCGAGGGTGTCCAGCTAA		
			CAGCGGCTCAAGAACTAATGATCCAGCAGTT		
			GGTGGCGCCCAACTGCAGTGCAACAAACG		

				CTCCTTCTCCGACCAGCCCAAAGTCACGCCC TGGCCCCTGGGCGCAGACCCCCAGTCCCGA GATGCCCGCCAGCCACCTTTGCCCACTTCA CGGAGCTGGCCATCATCTCAGTCCAGGAGAT CGTGGACTTCGCTAGCAGTCCTGGTTTC CTGCAGCTGGCCGGGAGGATCCCTGTTTC CTGCAGCTGGCCCGGGAGGATCATC CTCCTGAAGCATCCACTATCGAGATCATGC TGCTAGAGGCATCCACTATCGAGATCATGC TGCTAGAGACAGCCAGGCCTACAACCACGA		
Shigella ospD1	8		54		255	MKDEPRSTNLFMKLDSVFIWK EPFGLVLIIAPWNYPLNLTLVLL VGTLPAGNCVVLKPSEISQGT EKVLAEVLPQYLDQSCFAVVL GGPQETGQLLEHKLDYIFFTG SPRVGKIVMTAATKHLTPVTLE L
Shigella ospD1	2	prey67648	55	GCTGGGGATCGCGCTGGCGCTCCTGGGCGGA GAGGCTTCTGGCACTCAGAATCGACTTAAA GCCTCCAGAGAAGTAGAATCTGTAGACCTTC CACACTGCCACTGATTAAAGGAATTGAAGC TGGCTCTGAAGATATTGACATACTTCCCAATG GTCTGGCTTTTTTTTAGTGTGGGTCTAAAATTC CCAGGACTCCACAGCTTTGCACCAGATAAGA CTGGAGGAATACTAATGATGAATC AGAAAAACCAAGGCACCGGGAATTAAGAATC AGAAAAACCAAGGCACCGGGAATTAAGAATC AGACAAGGGCACCGGGAATTAAGAATC AGTCGTGGGTTTGATTTGGCCTCATTCAATCC ACATGGCATCAGCACTTTCATAGAATC	256	LGIALALGERLLALRNRLKAS REVESVDLPHCHLIKGIEAGSE DIDILPNGLAFFSVGLKFPGLH SFAPDKPGGILMMDLKEEKPR ARELRISRGFDLASFNPHGIST FIDNDD
Shigella	3	prey67266	26	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	257	XXXXXXXXXXXXXXXXXX

ospC1				NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN		XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Shigella ospC1	м	prey67267	57	TCAGTAGGCATAGT SCAATAGACATATAA TCCATATAAATGATT GAAATTATTTATGT GATGCCATCNGATT STGNGNCTANNGAN NTNCTNNGGCNTNG NTNGNCNNNGTTGTT CGGNGNCNGTTGAT CGGNGNCNGTTGAT	258	YYLLDVSVGIV*RYVVCNRHIN DLFTLLHINDLFV*CLGNYFMS YGC*FCCHXITTIXKIXXXXXXX YGC*FCCHXITTIXKIXXXXXXXX FELXLXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Shigella ospC1	m	prey50590	88	GTTTGATCAGCGTCAGGAATACTTCATGGAGGTCA TTGACATTCAATCAAGGGGGGTCA ACAAGGAGTTCACCGTGAACGGGGGGTCA ACAGGCGCTGCAAGGGGGGACGA GTGTGAGCGCTGCAAGGGGGAACGA GCTGGCGCCCCAAGGTGCAGCATTGCCATCAT CTGTGGCCGCTTTTGTGATGCGTTCCACGTGTA ACAGGCCCTTTTGTGATGCGTTCCACGTGTA ACAGGCCCTTTTGTGATGCGTCCATCATCAT ACAGGCCCTTTGTGGTCTGCGGGGAGCAGG ATCGCCTGTGTGGTCTGCAGGGAGGGAG ACCGTGAGGAAAAAGGGGAA ATTTCATTACGTTCAGGGTGCAGGAAAAGGCC CTGTGTTCCGGAGGGGGGAAAAAGGGCA ATTTCATTACGTTCAGGGAGAAAAGGCC CTGTGTTCCGGAGGGAGCAGCC CTGTGTTCCGGAGGGACAAAAGGGGAA ATTTCATTACGTTCAGGGTGCAGGCT	259	FDQPQEYFMELTFNQAAKGV NKEFTVNIMDTCERCNGKGNE PGTKVQHCHYCGGSGMETIN TGPFVMRSTCRRCGGRGSIIIS PCVVCRGAGQAKQKKRVMIP VPAGVEDGQTVRMPVGKREIF ITFRVQKSPVFRRDGADIHSDL FISIAQALLGGTARAQGLYETI NVTIPPGTQTDQKIRMGGKGI NVTIPPGTQTDQKIRMGGKGI PRINSYGYGDHYIHIKIRVPKRL TSRQQSLILSYAEDETDVEGT VNGVTLTSSGGSTMDSSAGS KARREAGEDEEGFLSKLKKMF TS*

	MADLLDSPALSGVQQFSGV GGGRCSEISAELIRSLTELQEL EAVYERLCGEEKVVERELDAL LEQQNTIESKMVTLHRMGPNL QLIEGDAKQLAGMITFTCNLAE NVSSKVRQLDLAKNRLYQAIQ RADDILDLKFCMDGVQTALRS EDYEQAAAHIHRYLCLDKSVIE LSRQGKGGSMIDANLKLLQEA EQRLKAIVAEKFAIATKEGDLP QVERFFKIFPLLGLHEEGLRRF SEYLCKQVASKAEENLLMVLG TDMSDRRAAVIFADTLTLLFEG IARIVEAHQPIVETYYGPGRLY TLIKYLQVECDRQVEKVVDKFI KQRDYHQQFRHVQNNLMRNS TTEKIEPRELDPILTEVTLMNA RSELYLRFLKKRISSDFEVGDS MASEEVKQEHQKCLDKLLNN CLLSCTMQELIGLYVTMEEYF MRETVNKAVALDTYEKGQLTS SMVDDVFYIVKKCIGRALSSSS
CTTCTTGGGGGAACAGCCAGAGCCCAGGGC CTGTACGAGACCACGTGACGATCCCCC CTGGGACTCAGACCAGAAGATTCGGAT GGGTGGGAAAGGCATCCCCCGGATTAACAG CTACGGCTACGGAGCCACTACATCCACATC AAGATACGAGTTCCAAAGAGGCTAACGAGC GGCAGCAGAGCCTGATCCTGAGCTACGCCG AGGACGAGACCTTGAACGAGCG AGGCGTCACCCTCACCAGGGGGGACGGTGA ACGCCGTCACCCTCCCCAGGAGCAAGG CTAGGCGTGAGCTCGGCGGAGGGGGGGGGG	ATGGCGGACCTTGATTCGCCTCCGAAGCTGT CAGGGGTGCAGCCGTCTGAGGGGGTGG GAGGTGCCGCTCCCAAATCTCCGCTG GAGGTGCCCCTCGCACAATCTCCGCTG ACCTCATTCGCTCCCTGACAGGCTGCGG CCGAGGAAAGTGCTGCAGGACTGGAA GCTGGAGGCTGTATACGAACGGCTCTGCGG CCGAGGAAAGTGGTCAATGGAGCTGCAATGGGTCC TAATCTGCAACGCAATGACCAATGGGTCC TAATCTGCAGCTGATTGAGGAAACCCCTTTACCTGCA CCTGGCTGGAATGATCACCCTTTACCTGCA ACCTGGCTGAATGTGTCCAGCAAAGTCG TCAGCTTCAGAATGTGTCCAGCAAAGTCG TCAGCTTCAGAATGTTTTTAGGAATGTTTTTTTTTT
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TGAGGAATCTGCTCATGGTCTGGGACA GACATGAGTGATCTTCTTTCTTTCTTTTCAGGAGGACATCT TTGCAGATACACTTACTCTTTCTTTTGAGGAGACTCTTTTTTTT	
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TTGCGGATACTTTCTGTTTGAGGGCAGGGGGAGGG ATTGCCCGCATTGTGGGCCAGCGGCAGGGAGTC TAGTGGAGCCTATTATGGGCCAGCGGAGGTC TAGTGGAGCCTATTATGGGCCAGGGAGTC CTATACCCTGATCAAATATCTGCGGTGAGAC AGTTCTACAGCAAGGGAAGGG	
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TAGTGGAGACTATTATGGGCCAGGGAGACT CTATACCCTGATCAAATATCTGCAGGTGGAAT GTGACAGACAGGGACAGCGAAA GTTCATCAAGCAAGAACAACCCTGATGAGA AATTCTCAACAAGAACAACCCTGATGAGA AATTGTCAACCAACAGAACACCCTGATGAGA ACTGGACCCCATCCTGACTATACTTACCTTAC	
CTATACCCTGATCAAGAGAAGGTGGTAGAAT GTGACAGACGGTGGAAGAGTGGTAGACA AGTTCATCAAGCAAAGGGACTGCTGATGAGA AATTCTACAAGAAAAATCGAACCAGAGA AATTCTACAAGAAAAATCGAACCAGAGA ACTGAACACCCCATCCTGAAGAGTTATCTTTGAG GTGGACCCCCATCCTGAGGTTATATTTGACTTACCTTGA AGCAGAGACTCCTTATATTTTGACATACTTACATAC AGCAGAGACTCTTATATTTTACTTACCATGA AGCAGACTCTTATATTTACTTACCATGA AGCAGACTCTTATATTTACTTACCATGA AGCAGCTCTTATAGTTACTTACCATGA AGCAGACTCTTATAGTTACTTACCATGA AGCAGCTCTTATAGTTACTTACCATGA AGCAGCTCTTATAGTTACTTACCATGA AGCAGCTCTTATAGTTACTTACCATGA AGCAGCTCTTATAGTTACCATGAC AGCATACTTCTTAGACTGCTTAAAA AGCAGCTCTTATAGTTACTTACCATGA AGCATACTTCTTAAGAAGTGCT ACTACATTTGTTAAGAAGTGCTTCTTTA AGCATTCTTAAGAAGTGCTTCTTTATA AGCATTCATCATCAGACAAGTGCT AGCACATCCAGCATTGACAAGTGCT AGCACATCCAGCACTCTCTTTATATACT AGCACATCCAGCACTCTCTTTAAAAAGTGCT AGCACATCCAGCACCACCACAAGTGCT AGACATTCACACCTCCGCCACCACAAGTGCT AGACATCCACCACCACCACAAGTGCT AGACATTCACACACACACAGAGCCT AGACATCCACACACACACAGAGCCT AGACATTCACACACACACACAGAGCT AGACATTCACACACACACACAGAGCT AGACACACCACAC	
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ACTGGACCCCATCCTGACTGAGGTTACCTGATTACGCT TCCTCAAGAAGAGGATTAGCTTACGCT TCCTCAAGAAGAGGATTAGCTTTGAG GTGGGAGACTCCATGGCCTCAGAGGAGTAA AGCAAGAGCACCAGAAGTGTCTGGAAGTAACTGCCTTTTGAGCTGTACATGC CCTCAATAACTGCCTTTTGAGCTGTACATGGA AGGAGCTAATTGGCTTATATGTTACCATGGA AGGAGTACTTCATGAGGAGACTGTCAATAAG GGAGTACTTCATGAGGAGACTGTCAATAAG GCATCGTCGCTCTGGAGGACTGTCAATAAG GCATCGTCGCTCTGGAGAGGCC CAGCTGACATCCAGCACTGTGAGAGGCC CAGCTGACATCATGAGAGGCCACCAGAGGCC CAGCTGACATCATGATGACTGTTAAGAGGCC CAGCTGACATCATGATGAGAGGCCTCTGT TCTACATTGTTAAGAAGTGCATTGGTGAATAAG GCCATGATCAACCTCGCCACCACAGAGCTGC TCTACATTGTTCAGGGATGTCTTTTTTTTTT	
ATGAACGCCCGCAGTGAGCTATACTTACGCT TCCTCAAGAAGAGGGATTAGCTCTGATTTTGAG GTGGGAGACTCCATGGCCTCAGAGGAAGTAA AGCAAGAGCACCCAGAAGTGTCTGGACAACT CCTCAATAACTGCCTTTTGAGCTGTACCATGC AGGAGTACTTCATGAGAGCTGTACATGGA GGAGTACTTCATGAGAGGCCTGATAAG GCTGTGGCTCTGGACACTGTCATGAGAGGCC CAGCTGACATTCATGAGAGGCCTTATAGAAGGCC CAGCTGACATTCATGAGAAGTGCTTCATGAGAAGGCC CAGCTGACATCCAGCATTGTTAAGAAGGCC CAGCTGACATCAGCACCCTTTGATAAGAAGGCC CAGCTGACATCAGCACCCACCACAGAGCCC TCTACATTGTTAAGAAGTGCATTGTGATAAGA GCCATGATCAACTCCAGCACTGCTGTTCTGT TCTGTCCAGCTCCAGCACTGCCACCACAGGCCC AGGACATCAACTCAGCACACAGGCCGCCTTCC AGGACATCCAGCACAGGCACCACGCAAGGCCCTCCAGCAAGGCTCCAGCAAGGCTTCCTGTTCTTCTTGTTAATAAGCCATTCATGCACAAGGCCTCCAGCAAGGCTTCCTGGTGACTTCTTGAACAAAAGGCATCGAGAGTACTCAGCAAAAAGGCATCGAGAGATTTGAACAAAAGGCATCCTGGAAAAACGCATCGGAAAAACGCATCCTGGAAAAACATCCTTGAAAAACGCATCCTGGAAAAACATCCTTGAAAAACATCCTTGAAAAACATCCTTGAAAAACATCCTTGAAAAACACTCCTGGAAAAACATCCTTGAAAAACACTCCTGGAAAAACATCCTTGAAAAACACTCCTGGAAAAACATCCTTGAAAAACACTCCTGGAAAAACATCCTTGAAAAAACACTCCTGGAAAAACATCCTTGAAAAACACTCCTGCAAAAAACATCCTTGAAAAAACACTCCTGGAAAAACATCCTTGAAAAAACACTCCTGGAAAAACATCCTTGAAAAAAACACTCCTGGAAAAACATCCTTGAAAAAAACACTCCTGCAAAAAACAAAAAAAA	
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GTGGGAGACTCCATGGCCTCAGGAGGAAGTAA AGCAAGAGCACCAGGAGTGCTGGACAACT CCTCAATAACTGCCTTTTGAGCTGTACCATGGA AGGAGCTAATTGGCTTATATGTTACCATGGA GGAGTACTTCATGAGGGGAGACTGTCAATAAG GGAGTACTTCATGAGGGGACTGTCAATAAG GGAGTACTTCATGAGGGGACTGTCAATAAG GCTGTGGCTCTCGACCATGGTGGTGGTGTCT TCTGCTGACTTCATGAGAAGTGCTTCTGT TCTGCTCAGCTCCAGCATTGATGATAAG TCTGCTCAGCTCCAGCATTGTTAAGAAGGCC CAGCTGACTTCAGCACCACAGAGCTGT TCTGCTCCAGCTTCCTGCTGTTCTTTTT TCTGCTCAGCTTCCAGCACTGTTCTTTTT TCTGCTCAGCTTCCTGCCAGAGCTGC AGGACATCCAGCGCACCCCCCCCCC	GAGGATTAGCTCTGATTTTGAG VLALRIDFRSEDIKRLRL*
AGCAAGAGCACCAGAAGTGTCTGGACAAACT CCTCAATAACTGCCTTTTGAGCTGTACCATGG AGGAGCTAATTGGCTTATATGTTACCATGGA AGGAGCTACTTCATGAGGGAGACTGTCAATAAG GGAGTACTTCATGAGGGAGACTGTCAATAAG GCTGTGGCTTCATGAGAGGGC CAGCTGACATCCTAGAGAAGGCC CAGCTGACATCCTATGATAGGAAGGGC CAGCTGACATCATGATGGTGAATAAG TCTGTCCAGCTCCAGCATTGTTAAAGAAGGCGGC AGGACATCAACCTCCCACCACAGAGCTGG AGGACATCCAGCGCACCACAGAGCTGC AGGACATCCAGCGCACCACAGAGCCG AGGACATCCAGCGCGGGTGAAAAGGCCTTCC AGGACATCATGCACAGAGGCGAGGC	rccatggcctcagaggaagtaa
CCTCAATAACTGCCTTTTGAGCTGTACATGGAAGGGAGGTACTTCATGAGGAGGAGCTGTTACCATGGAGGGAG	4CCAGAAGTGTCTGGACAAACT
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GGAGTACTTCATGAGGGAGACTGTCAATAAG GCTGTGGCTCTGGACACCTATGAGAAGGGC CAGCTGACATCCAGCATGGTGGATGATGTCT TCTACATTGTTAAGAAGTGCATTGGGCGGGC TCTACATTGTTAAGAAGTGCATTGGGCGGGC TCTGTCCAGCTCCAGCATTGTCTTCTGTGTGTAAAG GCCATGATCAACCTCGCCACCACAGAGCTGG AGTCTGACTTCAGGGATGTTCTGTTAATAAG CTGCGGATGGGCTTTCCTGCCACCACCTTCC AGGACATCCAGCGCGGGGTGACAGTGCCG CAAATTTGACACAAAGGCGTGACAGGCGCGCGGGAGTACT GAACATTTGACACAAAAGGCGAGGTGACT TGAACATCGGAAAAGGCCTCCTGGGGAGGTGCT TGAACAACGTGGAAGAGTGCTCCTGGTGAAAACAT TGAACAACTTGAAGAAGATTGCAGCAGTGAAAACAT TGAACAACGTGGAAGAACAT TGAACAACGTGGAAGAACAT	TGGCTTATATGTTACCATGGA
GCTGTGGCTCTGGACATCTATGAGAAGGGC CAGCTGACATCCAGCATGGTGGATGATGTCT TCTACATTGTTAAGAAGTGCATTGGGCGGC TCTGTCCAGCTCCAGCATTGACTGTTCTGT GCCATGATCAACCTCGCCACCACAGAGCTGG AGTCTGACTTCAGGGATGTTCTGTGTAATAAG CTGCGGATGGGCTTTCCTGCCACCACCTTCC AGGACATCCAGCGCGGGGTGACAGTGCCG TGAACATTGACACAAAGTGCCG CAATTTGACACAAAGGCGTGAAGTGCT GACATTTGACACAAAGGCGTGAGGTGACT TGAACATGGAAAAGGCATCGGGGAGTGCT TGAACAGGGGAAGATTCTGCAGTGAAAACAT	;ATGAGGGAGACTGTCAATAAG
CAGCTGACATCCAGCATGGTGGATGATGTCT TCTACATTGTTAAGAAGTGCATTGGGCGGGC TCTGTCCAGCTCCAGCATTGACTGTTCTGT GCCATGATCAACCTCGCCACCACAGAGCTGG AGTCTGACTTCAGGGATGTTCTGTGTAATAAG CTGCGGATGGCTTTCCTGCCACCACCTTCC AGGACATCCAGCGGGGGTGACAGTGCCG TGAACATTGACACAGAGGCGTGAAGTGCCG TGAACATTTGACACAAAAGGCATCGAGAAGG TGAACATTTGACACAAAAGGCTTCCTGGTGAAGTGCT TGAACATTTGACACAAAAGGCATCGAGAGTGACT TGAACAGGGGAAGATGTCCTTCCTGGTGAAAACGTTGACATGGAAAACAT TGAACAACGTGGAAGATGCCTTCCTGGTGAAAACAT TGAACAACGTGGAAGATGCCTTCCTGGTGAAAACAT TGAACAACGTGGAAGAACAT	STGGACACCTATGAGAAGGGC
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GCCATGATCAACCTCGCCACCACGAGGTGTGGATGTTCTGTGTAATAAGAGTCTGCGGATGTTCTGTGTAATAAGCTGCGGATGTTCCTGCCACCACCTTCCAGCGATGCTTCCTGCCACCATTCCAGCGCGCGGGGTGACAAGTGCCGGGGTGACAAGGCCTTCCAGCGCAAGGGCAAGGGCATCGAGCAAGGGCATCGAGGAAGGCATCGAGGAAGGTGCTTCCTGGTGACTCTGAACAAAGGCATCGGTGAACATTGACAAAAGGCATCGAGTGACTTGAACAAAAGGCATCGGTGACTCTGAACAAAAGGCATGGAAAAACATTGAACAAAAGGAAGAAAACATCCAACTGGAAGAAAACATCCAACTGAAGAAAACATCCAACTGAAGAAACATCCAACTGAAGAAGAACATCCAACTGAAGAAACATCCAACTGAAGAAAACATCCAACTGAAGAAGAACATCCAACTGAAGAAGAACATCCAACTCGAAGAAGAACATCCAACTCTGAAGAAGAACATCCAACTCGAAGAAACATCCAACTCGAAGAAGAACATCCAACTCGAAGAAACATCCACTCGAAGAAACATCCACTCGAAGAAACATCCACTCGAAGAAGAACATCCACTCGAAGAAACATCCACTCGAAGAAACATCACACTCCAACTCGAAGAACATCACACTCCACTCGAAGAACACTCCACTCGAAGAACATCACACTCCACTCGAAGAACATCACACTCCACTCGAAGAACACTCCACTCGAAGAACACTCCACTCGAAGAACACTCCACTCGAAGAACACTCCACTCGAAGAACACTCCACTCGAAGAACACTCCACTCGAAGAAACACTCCACTCCACTCGAAGAACACTCCACTCCACTCCACACACA	STCCAGCATTGACTGTCTGT
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				ATTCCGAGACCTCTTGCAGGAAGGGGTGACG GAGCTCAACAGCACAGC		
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				AAATCCACCTTTAACCGGCTGGGTGGTGGTGGCTGC AGTTTGACAAGGAGCTGAGGTCGCTCATTGC CTACCTTACCACGGTGACCACCTGGACCATC CGAGACAAGTTTGCCCGGCTCTCCAGATGG	***	
				CCACCATCCTCAATCTGGAGCGGGTGACCGA GATCCTCGATTACTGGGGACCCAATTCCGGC		
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	GCGCCACGTACATGGACCAGGCCCCTCCC	
	CAGCTGTGTCCCCAGGCTCACTATAACAT	
	GTACCCACAGAACCCTGACTCAGTCCTTGAC	
	ACCGATGGGGACTTCGATCTGGAGGACACAA	
	TGGACGTAGCGCGCGTGTGGAGGAGCTCC	

				TGGGCCGGCCAATGGACAGTCAGTGGATCC		
				CGCACGCACAATCGTGA		
Shigella	3	prey700	63	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGA	264	MGIGLSAQGVNMNRLPGWDK
ospC1		•		ACATGAATAGACTACCAGGTTGGGATAAGCA		HSYGYHGDDGHSFCSSGTGQ
				TTCATATGGTTACCATGGGGATGATGGACATT		PYGPTFTTGDVIGCCVNLINNT
				CGTTTTGTTCTTCGGAACTGGACAACCTTAT		CFYTKNGHSLGIAFTDLPPNLY
				GGACCAACTTTCACTACTGGTGATGTCATTG		PTVGLQTPGEVVDANFGQHP
				GCTGTTGTGTTAATCTTATCAACAATACCTGC		FVFDIEDYMREWRTKIQAQID
				TTTTACACCAAGAATGGACATAGTTTAGGTAT		RFPIGDREGEWQTMIQKMVS
				TGCTTTCACTGACCTACCGCCAAATTTGTATC		SYLVHHGYCATAEAFARSTDQ
				CTACTGTGGGGCTTCAAACACCAGGAGAGT		TVLEELASIKNRORIQKLVLAG
				GGTCGATGCCAATTTTGGGCAACATCCTTTC		RMGEAIETTQQLYPSLLERNP
				GTGTTTGATATAGAAGACTATATGCGGGAGT		NLLFTLKVRQFIEMVNGTDSE
				GGAGAACCAAAATCCAGGCACAGATAGATCG		VRCLGGRSPKSQDSYPVSPR
				ATTTCCTATCGGAGATCGAGAAGGAGAATGG		PFSSPSMSPSHGMNIHNLASG
				CAGACCATGATACAAAAATGGTTTCATCTTA		KGSTAHFSGFESCSNGVISNK
			_	TTTAGTCCACCATGGGTACTGTGCCACAGCA		AHQSYCHSNKHQSSNLNVPE
				GAGGCCTTTGCCAGATCTACAGACCAGACCG		LNSINMSRSQQVNNFTSNDVD
				TTCTAGAAGAATTAGCTTCCATTAAGAATAGA		METDHYSNGVGETSSNGFLN
				CAAAGAATTCAGAAATTGGTATTAGCAGGAA		GSSKHDHEMEDCDTEMEVDS
				GAATGGGAGAAGCCATTGAAACAACACACA		SQLRRQLCGGSQAAIERMIHF
				GTTATACCCAAGTTTACTTGAAAGAAATCCTA		GRELQAMSEQLRRDCGKNTA
				ATCTCCTTTTCACATTAAAAGTGCGTCAGTTT		NKKMLKDAFSLLAYSDPWNSP
				ATAGAAATGGTGAATGGTACAGATAGTGAAG		VGNQLDPIQREPVCSALNSAIL
				TACGATGTTTGGGAGGCCGAAGTCCAAAGTC		ETHNLPKQPPLALAMGQATQ
				TCAAGACAGTTATCCTGTTAGTCCTCGACCTT		CLGLMARSGIGSCAFATVEDY
				TTAGTAGTCCAAGTATGAGCCCCAGCCATGG		*±
				AATGAATATCCACAATTTAGCATCAGGCAAAG		
				GAAGCACCGCACATTTTCAGGTTTTGAAAGT		
			-	TGTAGTAATGGTGTAATATCAAATAAAGCACA		
				TCAATCATATTGCCATAGTAATAAACACCAGT		
				CATCCAACTTGAATGTACCAGAACTAAACAGT		
				ATAAATATGTCAAGATCACAGCAAGTTAATAA		
				CTTCACCAGTAATGATGTAGACATGGAAACA		
				GATCACTACTCCAATGGAGTTGGAGAAACTT		

40.400 4-0-4-	GATCGAGATCCATGGGAAGGCAGGCCTGTTT 265 IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFFELEGY IEHHGKAGLFLEGGINFGFE IEHHGKAGLFLGGYSEGY IEHHGKAGLFGGASPLITYFTDDKGA YSVGPLHSDLEYTYTSQKEGY IEHHGKAGASPLITYFTDDKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAYALAGVSE IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKAGASPLITYFTDGKGAS IEHHGKASPTYTTGTGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CATCCAATGGT CATGACCACGA AAATGGAAGTTG CCAGTTGTGTG GAAAGAATGAT AAGCAATGACA AAGGATGCATT TCCCTGGAACA GACCCGATTCA CTCCTCAAAGCA TCCCTGGAACA GACCCGATTCA GACCCGATCA GACCCGATCA GGCCCGATCA GGCCCGATCA GGCCCGATCA GGCCCGATCA	GATCGAGATCC TTAGAAGGCCA GAGTCGAGATT AAGTTCACCGC ACAAAGGTGCCTAGGGCTA GACCATCGGAGGCTAA GACCATCGGAGCCTAACCATCAAGAGGCGCTTAAACCGCTTAAACGGCTTACCAAGAGGCTTACGAAGGCTTACGGAAGGCTTAAACGGGCTTAACGGGGCTTAACGGGGCTTAACGGGGCTTAACGGGGCTTAACGGGGCTTAACGGGGCTTAAACGGGCTTAAACGGGGCTTAACGGCATTAAACGGCATTAAACGG
	4
	prey3486
	က
	Shigella ospC1

			AAGAGGCCAAGTTCAGATTACGTGGATTGCT GCCGGGATGTGTGTACCACGTTCAGCTCAAG		
			GCAGAAGGCAACGACCACATTGAGCGGGCG		
			CTCCCCCACCATAGGGTGATTGAGGTTGGGA		
			ATAATGACATCGATGATGTAAACATCATAGTT		
			TTCCGGCAGATTAATCAATTTGATTTAAGTGG		
			AAATGTGATCACTTCCTCTGAATACCTTCCTA		
			CATTATGGGTCAAGCTTTACAAAAGCGAAAAC		
			CTCGACAATCCAGACAGTTTCCCTTG		
			GCCAGTCCCTGTTCTTCCCCCCCACT		
			GCTCAGAGACGGCGAACTATGTIGTIGT		
			CIGGACICCACACICCCAGIAIG		
			GTGGGCTACCATAAACACACCACCTTGATTTT		
			TAATCCCACGAGGAAGCTGCCTGAACAGGAC		
			ATCGCACAAGGATCCTACATTGCCCTGCCAT		
			TGACGCTGCTGGTTCTGCTGGCCGGTTACAA		
			CCATGACAAGCTCATTCCTTTGCTGCTGCAG		
			TTGACAAGCCGGCTACAGGGAGTCCGCGCG		
			CTCGGCCAGGCAGCCTCTGACAATAGCGGC		
			CCAGAAGATGCAAAGAGACAAGCCAAGAAAC		
-			AGAAGACAAGGCGGACTTGA		
Shigella 3	prey14801	65	CCTGGGCCTACATTCTCCCATTGCCCTAGAT 266	IGCHSPI	LGLHSPIALDVLSEAFEESLVA
ospC1			GTACTGAGTGAGGCTTTTGAGGAATCCTTGG	RDWSRA	RDWSRALQLTEVYGRDVDDL
			TGGCCAGAGATTGGTCCCGGGCCCTTCAGCT	SSIKDAV	SSIKDAVLSCAVAYDKEGWQY
			CACTGAAGTGTACGGGCGAGATGTGGACGAT	LFPVKD/	LFPVKDASLRSRLALQFVDRW
			TTGAGCAGCATAAAGGATGCAGTCCTGAGCT	PLESCLE	PLESCLEILAYCISDTAVQEGL
			GTGCTGTGGCATATGACAAAGAAGGTTGGCA	KCELORI	KCELQRKLAELQVYQKILGLQ
			ATACCTGTTTCCCGTGAAGGATGCATCTCTG	SPPVWC	SPPVWCDWQTLRSCCVEDPS
			AGAAGTCGGCTGGCCCTACAGTTTGTGGACA	TVMNMIL	TVMNMILEAGEYELCEEWGCL
			GETGGCCCCTGGAGTCATGCCTGGAGATTCT	YPIPREH	YPIPREHLISLHQKHLLHLLER
			GGCCTACTGCATTTCAGACACGGCTGTCCAA	RDHDKA	RDHDKALQLLRRIPDPTMCLE
			GAAGGACTAAAGTGTGAGCTACAGAGGAAGC	VTEQSLI	VTEQSLDQHTSLATSHFLANY
			TGGCGGAGCTGCAGGTGTATCAGAAGATTCT	LTTHFY	LTTHFYGGLTAVRHREIQALYV
			GGGTTTGCAGTCTCCCCCAGTGTGGTGTGAC	GSKILLTI	GSKILLTLPEQHRASYSHLSSN

	TGGCAGACCTTGAGGAGCTGTTGTGTTGAGG	PLFMLEQLLMNMKVDWATVA
	ACCCATCAACTGTCATGAACATGATTCTAGAA	VQTLQQLLVGQEIGFTMDEVD
	GCACAGGAGTATGAACTGTGAAGAGTGGG	SLLSRYAEKALDFPYPQREKR
	GCTGCCTGTACCCCATTCCAAGAGAACATTT	SDSVIHLQEIVHQAADPETLPR
	AATCAGCCTTCATCAAAAGCATCTTCTCCACC	SPSAEFSPAAPPGISSIHSPSL
	TTCTAGAAAGAAGATCATGACAAGGCTCT	RERSFPPTQPSQEFVPPATPP
	GCAACTCCTGCGAAGAATCCCTGACCCCACC	ARHOWVPDETESICMVCCRE
	ATGTGCCTTGAAGTGACAGAGCAATCCCTCG	HFTMFNRRHHCRRCGRLVCS
	ACCAGCACATAGCTTGGCCACTTCTCACTT	SCSTKKMVVEGCRENPARVC
	CTTGGCCAACTACCTCACCACCCACTTCTAT	DQCYSYCNKDVPEEPSEKPE
	GGACAACTGACTGCTGTCCGACACCGTGAAA	ALDSSKSESPPYSFWRVPKA
	TCCAGGCGCTGTATGTGGGATCCAAGATTCT	DEVEWILDLKEEENELVRSEF
	GCTGACCCTGCCTGAGCAGCACCGGGCCAG	YYEQAPSASLCIAILNLHRDSIA
	CTATTCCCACTTGTCCTCTAACCCCCTGTTCA	CGHQLIEHCCRLSKGLTNPEV
	TGCTGGAGCAGCTGCTTATGAACATGAAGGT	DAGLLTDIMKQLLFSAKMMFV
	GGATTGGGCCACTGTGGCTGTGCAGACTCTC	KAGOSODLALCDSYISKVDVL
	CAGCAGCTGCTGGTTGGACAGGAGATTGGCT	NILVAAAYRHVPSLDQILQPAA
	TCACTATGGACGAGGTGGACTCACTGCTTTC	VTRLRNQLLEAEYYQLGVEVS
	CAGATACGCAGAGAAGCCCTGGACTTTCCA	TKTGLDTTGAWHAWGMACLK
	TACCCTCAGAGGGAGAAACGATCAGATTCTG	AGNLTAAREKFSRCLKPPFDL
	TGATTCACCTCCAAGAAATTGTCCACCAGGC	NOLNHGSRLVQDVVEYLESTV
	TGCAGATCCCGAGACCCTCCCTAGATCACCA	RPFVSLQDDDYFATLRELEA1
	TCAGCAGAGTTCTCCTGCTGCTCCTCGTG	LRTQSLSLAVIPEGKIMNNTYY
	GTATCTCCAGTATACATTCCCCTAGTCTAAGG	QECLFYLHNYSTNLAIISFYVR
-	GAAAGGAGTTTCCCACCAACCCAGCCCTCAC	HSCLREALLHILNKESPPEVFI
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	CAGGCACCAGTGGGTACCGGATGAGACTGA	IDPTLESWGKYLIAACQHLQKK
	GAGTATCTGCATGGTCTGCTGCAGGGAGCAC	NYYHILYELQQFMKDQVRAAM
	TTCACCATGTTTAACAGGCGTCATCATTGTCG	TCIRFFSHKAKSYTELGEKLS
	CCGCTGTGGCCGGCTAGTGTGCAGCTCCTG	WLLKAKDHLKIYLQETSRSSG
	CTCCACTAAGAAATGGTGGTTGAAGGCTGC	RKKTTFFRKKMTAADVSRHM
	AGAGAACCCTGCTCGTGTGTGATCAGT	NTLQLQMEVTRFLHRCESAGT
	GCTATAGTTACTGCAACAAAGATGTACCAGA	SQITTLPLPTLFGNNHMKMDV
	GGAGCCTTCAGAAAACCAGAAGCTCTAGAC	ACKVMLGGKNVEDGFGIAFRV
	AGCTCCAAGAGTGAAAGCCCTCCATACTCGT	LODFOLDAAMTYCRAARQLV
	TTGTGGTGAGAGTCCCCAAAGCAGATGAGGT	EKEKYSEIQQLLKCVSESGMA

AKSDGDTILLNCLEAFKRIPPQ ELEGLIQAIHNDDNKVRAYLIC	CKLRSAYLIAVKQEHSRATALV	QQVQQAAKSSGDAVVQDICA	QWLLTSHPRGAHGPGSRK*																															
GGAATGGATTTTGGATCTCAAAGAGGGGAA	AGCAGGCCCCAGCGCCTCCTTGTGCATTGC	CATCCTGAATCTGCACCGGGACAGCATTGCC	TGTGGTCACCAGCTGATTGAGCACTGCTGCA	GGCTCTCCAAGGGCCTCACCAACCCAGAGG	TGGATGCCGGGCTGCTCACGGACATCATGAA	GCAGCTGCTGTTCAGCGCCAAGATGATGTTC	GTCAAAGCCGGCCAGAGCCAAGACTTGGCT	CTTTGTGACAGCTACATCAGCAAGGTAGATG	TGCTGAATATTTTAGTTGCTGCTGCCTATCGC	CACGTGCCATCTTTGGATCAGATCTTGCAGC	CAGCTGCAGTAACCAGGCTAAGGAACCAGCT	TTTGGAAGCCGAGTACTACCAACTGGGCGTT	GAGGTCTCCACAAAGACTGGGCTTGATACCA	CCGGGGCGTGGCATGGGGCATGGCCT	GCCTCAAAGCCGGGAACCTCACTGCTGCAC	GGGAGAAGTTCAGTCGCTGTCTGAAGCCCCC	ATTTGACCTCAATCAGCTGAATCATGGCTCAA	GGCTGGTGCAGGATGTGGTTGAGTACCTAGA	GTCCACAGTGAGGCCCTTTGTATCCTTGCAA	GATGACGATTACTTTGCCACCCTGAGGGAAC	TGGAAGCTACCCTTCGGACGCAGAGCCTTTC	TCTGGCAGTGATTCCTGAAGGGAAAATCATG	AACAACACCTACTACCAGGAATGCCTCTTCTA	CCTGCACAACTATAGCACCAACCTGGCCATC	ATCAGCTTCTACGTGAGGCACAGCTGCCTGC	GGGAAGCTCTTCTGCACCTTCTCAACAAGGA	GAGTCCTCCAGAAGTTTTTATAGAAGGCATTT	TCCAACCAAGCTATAAAAGTGGGAAGCTACA	CACTTTGGAGAACTTGCTAGAATCCATTGATC	CAACCTTGGAGAGCTGGGGAAAGTACTTGAT	TGCTGCCTGCCAACATTTACAGAAGAAGAAC	TACTACCACATTCTGTATGAGCTGCAGCAGTT	TATGAAGGACCAAGTTCGGGCCGCCATGACC	TGTATTCGGTTCTTCAGTCACAAAGCAAAGTC
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				- CC * * FC * CF * FC		
				\exists		
Shigella	3	prey67280	29		268	NFHLPREVYVFF*ALFYVFTSL
ospC1				TTTCTAGGCCCTTTTCTATGTCTTTACATCTCT		SHTHTRIHTHSLFLIK*DYTTHIL
•				GTCTCACACACACACGTATACACACACAC		SLAFLLKSISKRILCVSEAGATS
		-		AGTTTATTTTAATAAATAGGATTATACCACA		FF*LAAWRSIECLSSCV*PSGW
				CACATCCTGTCACTTGCTTTTTGCTTAAGAG		IVCLFLVX
				TATATCTAAGAGAATCCTTTGTGTCAGTGAAG		
				CTGGAGCTACCTCATTCTTTAACTGGCTGC		
				GTGGCGTTCCATTGAGTGTCTGTCATGT		
				GTTTAGCCGAGTGGATGGATAGTCTGCTTGT		
Shinella	~	Drev40194	89	CAACCCCTTCTATGCCCCAAATCTC	269	NPVPL YAPNL SPPADSRIHVP
osnC1	,		3			ASGYCCLECGDAFALEKSLSQ
				CCGGCCAGTGGGTACTGCTGCCTGGAGTGT		HYGRRSVHIEVLCTLCSKTLLF
				GGAGACGCATTTGCCTTAGAGAAGAGCCTGA		FNKCSLLRHARDHKSKGLVM
				GCCAGCACTATGGCCGGCGGAGCGTCCACA		QCSQLLVKPISADQMFVSAPV
				TTGAGGTACTGTGCACACTGTGCTCCAAGAC		NSTAPAAPAPSSSPKHGLTSG
				GCTGCTCTTCAACAAGTGCAGCCTGCTC		SASPPPALPLYPDPVRLIRYS
				CGGCACGCCCGTGACCACAGAGCAAGGGG		IKCLECHKQMRDYMVLAAHFQ
				CTCGTCATGCAGTGTTCCCAGCTGCTGGTGA		RTTEETEGLTCQVCQMLLPNQ
				AGCCTATCTGCGGACCAAATGTTCGTGTC		CSFCAHQRIHAHKSPYCCPEC
				GGCCCCTGTGAACTCCACGGCACCAGCAGC		GVLCRSAYFQTHVKENCLHYA
				CCCAGCCCTTCATCCTCTCCCAAACATGGC		RKVGYRCIHCGVVHLTLALLK
				CTCACTTCGGGCAGTGCCAGTCCCCCTCCTC		SHIQERHCQVFHKCAFCPMAF
				CAGCCTTGCCACTCTACCCAGACCCTGTGAG		KTASSTADHSATQHPTQPHRP
				GCTCATCCGGTACTCAATCAAGTGTCTTGAAT		SQLIYKCSCEMVFNKKRHIQQ
				GTCACAAGCAGATGCGGGACTACATGGTCCT		HFYQNVSKTQVGVFKCPECPL
				GGCTGCACATTTCCAGAGGACAACAGAGGAG		LFVQKPELMQHVKSTHGVPR
				ACAGAGGGCTGACCTGCCAGGTATGCCAG		NVDELSNLQSSADTSSSRPGS
				ATGCTGCTGCCAACCAGTGCAGTTTCTGTG		RVPTEPPATSVAARSSSLPSG
				CCCACCAGCGGATTCATGCACACAGAGTCCCC		RWGRPEAHRRVEARPRLRNT
				CTACTGCTGCCGGAGTGTGGGGTCCTCTG		GWTCQECQEWVPDRESYVS
				CCGCTCTGCCTACTTCCAGACCCATGTAAAG		HMKKSHGRTLKRYPCRQCEQ
				GAGAATTGCCTGCACTATGCCCGCAAGGTGG		SEHTPNSLRKHIRNNHDTVKK
				GCTACAGGTGCATCCACTGTGGTGTCGTCCA		FYTCGYCTEDSPSFPRPSLLE

	CCTGACCTTGGCCTGAAAAGCCACATC	SHISI MHGIRNPDI SOTSKVKP
	CAGGAGCGACACTGCCAGGTTTTCCACAAAT	PGGHSPQVNHLKRPVSGVGD
	GTGCATTCTGCCCCATGGCCTTCAAGACTGC	APGTSNGATVSSTKRHKSLFQ
	CAGCAGCACTGCAGACCACGCACCCA	CAKCSFATDSGLEFQSHIPQH
	GCACCCAGCCCACAGACCCTCCCA	QVDSSTAQCLLCGLCYTSASS
	GCTCATTTATAAGTGCTCCTGTGAAATGGTCT	LSRHLFIVHKVRDQEEEEEE
	TCAACAAGAAGAGGCACATTCAGCAGCATTT	AAAAEMAVEVAEPEEGSGEE
-	TTACCAGAATGTCAGCAAGACGCAGGTGGGC	VPMETRENGLEECAGEPLSA
	GTCTTCAAGTGCCCTGAGTGCCCACTCTTGT	DPEARRLLGPAPEDDGGHND
	TCGTGCAGAAGCCGGAGTTGATGCAACACGT	HSQPQASQDQDSHTLSPQV*
	CAAGAGCACCCACGGTGTTCCCCCGAAATGTG	
	GACGAGCTGTCAAACCTCCAGTCTTCAGCGG	
	ACACATCCTCAAGCCGCCCTGGCTCTCGAGT	
	TCCCACTGAGCCACCAGCCACTAGTGTGGCT	
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	TGGGGTAGGCCTGAAGCCCACCGCAGGGTG	
	GAAGCCAGGCCGCGCTGAGGAACACTGGC	
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	ACAACCATGACACAGTAAAGAAGTTCTACAC	
	CTGCGGGTACTGCACAGAGGACAGCCCCAG	-
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	ATCAGCCTTATGCATGGCATCAGAAACCCTG	
	ATTTGAGCCAGACGTCCAAAGTGAAACCTCC	
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	CCAGGCACCAGCAATGGCGCAACTGTCTCTT	
	CCACCAAAAGGCACAAGTCCCTTTTCAGTG	
	CGCGAAATGTAGTTTTGCCACAGACTCGGGG	
	CTCGAGTTTCAGAGCCACATACCTCAGCACC	
	AGGTGGACAGCTCCACAGCCCAATGTCTCCT	
	CTGTGGTTTGTGCTACACCTCTGCCAGCTCC	
	CTCAGCCGCCACCTCTTGATGCCACAAGG	
	CTCAGCCGCCACCTCTTCATTGTCCACAGG	

				TGAGAGACCAGGAGGAGGAGGAGGAGGAGGG AGGCGCGCGC		
Shigella ospC1	ဇ	prey67287	69	L000 4L0	270	EHSSSLVMLFF*VCL*VGKVDL FGLA*GLNVSSSLGLLILSPSW LCGIMSLKQGE*SINILRRNILP TYVFYSSFF*ALSRKSNALAFN QK*KVY
Shigella ospC1	က	prey19931	2	GGTGCACCAAGTGACAGACCTTTCTAGAAAT 2 GCCCAGCTGTTCAAGCGCTCTTTGCTGGAGA TGGCAACGTTCTGA	271	VHQVTDLSRNAQLFKRSLLEM ATF*
Shigella ospC1	ო	prey67290	71	GGGGGGGTGGGGAGGTAATAACNN Z NATNTTCTTTTGGTANTNATACAGTGTGGNAN TCTCNTNTGAANNNTTCTATNGACNANAAATA TCTTTTTTTTTTTTTTTTTTTTTTT GTGGAGANGGCTGCTNTTTTTTTANNGNC TTTGTNTATTTTTCNTATTAGCAGAATATAN NNNNCTGNTNCTNCNATATTTTATGANATANN TGCTTNTAANCNTNTANAAATATT ATNNACTTNTTACATCATAGANNATATCT TT	272	GGVGMGR**XXXLLVXIQCGX LX*XXLXTXNIFFXSYLSXVFC GRXLLXFLXXLXIFXISRISAXL XLXYFMXXXLXXXXNLINIYXL XLHHIXXIF
Shigella ospC1	ဇ	prey67291	72	TTTGAAGGONTCNTANNAACATAGGANAATG Z TGGCTATAGTTTGGAACCTNCTACATATTTGT TGAATGGCTTTGACANACTTGCTGATAGTGAT	273	FEGXXXT*XNVAIVWNLLHIC* MALTXLLIVI*TLXSKLRWSQM EMRNLLGTEXQVTLVMFXPRP

ATGAACATTANNGTCCAAGCTGAGGTGGTCT CAAATGGAGATGAGGAACTG CAAATGGAGTGTTTTGTGGAACTG AAGNACAGGTGACTCTTTTTTTTTTTTTTTTTTTTTTTTT	73 GCACAAGCCGTCATACCATACCAGGCAGTAA 274 AQAVIPYQAVKIYSLVFFXK*IK AAATTTACTCCTTAGTTTTCTTCTANAAATAGA TTAAGTCTGTGATCCATTTTGGGTTAATTTTTC TGTGATGTATACTATTGTTTGAGGTTAATTTTTC TGTGATGTTTAAAAATTTTCATCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTTCCAGTTGTTTTCCAGTTGTTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTCCAGTTGTTTTCAGTTGTTCCAGTTGTTCCAGTTGTTTTTCAGTTGTTCCAGTTGTTTTTTTT	74 AGAGTGGGGATGGGCTCGTTTCGT 275 RVGMGWASVRPSDPHVCC CCGTCCGACCCCCTCATGTGCTGCCCCA AACCTCGCCGCCTCAGTTTGGTATTCTGT AACCTCGCCGCTCCTGGGGTAGTAGCTGACACCAG ACTCAGCTGGGTAGTAGCTGAGCTTTTC ACCCGGGTCGTTTTCCGACTTTTC ACCCGGGTCCTGGGGTCGTTTTCATCCAGGGTCGTTTTCATCCANAT TTAACCCGGGTCCTGTGCTTTTCATCCANAT TTAACCCGGGTCCTGTAGCTGCTTTTCATCCANAT TTAACCCGGGTCGTGCTTTTCATCCANAT TTAACCCGGGTCGTGCTTTTCATCCANAT TTGCTTCAGGG TTTTCATCCANAT TTGCTTCAGGG	75 CCTCCTCCAACACACACACACAGTGT 276 PPPPTHVHTVSAQCLLFFFKX CTGCCCAATGCCTACTTTTTTTTTTTTTTTTTTAANGA AANTTTNANTTNGNAANTANAANNNGGNTAAA ANGNCNTNNNCNTNTANCCTTTTNNNGTTTTT TTTNNTTTTTTTTTTTTTTTTTT
ATGA CAAA AGAC AGAC ANAT ATNC	_		
	prey67294	prey67296	prey67299
	Shigella 3 ospC1	Shigella 3	Shigella 3 ospC1

				TTTNAAGGTTTTNAAAAANNGTTTGGGA		
Shigella	3	prey4637	9/	AGT	277	QKDDKEPQPVKKTVTGTDADL
ospC1				GAAGAAGACAGTGACAGGAACAGATGCAGAC		RRLSLKNAKQLLRKFGVPEEEI
				CTTCGTCGCCTTTCCCTGAAAAATGCCAAGC		KKLSRWEVIDVVRTMSTEQAR
				AACTTCTACGTAAATTTGGTGTGCCTGAGGAA		SGEGPMSKFARGSRFSVAEH
		-		GAGATTAAAAAGTTGTCCCGCTGGGAAGTGA		QERYKEECQRIFDLQNKVLSS
				TTGATGTGGTGCGCACAATGTCAACAGAACA		TEVLSTDTDSSSAEDSDFEEM
				GGCTCGTTCTGGAGAGGGGCCCATGAGTAA		GKNIENMLQNKKTSSQLSRER
				ATTTGCCCGTGGATCAAGGTTTTCTGTGGCT		EEGERKELQRMLLAAGSAAS
				GAGCATCAAGAGCGTTACAAAGAGGAATGTC		GNNHRDDDTASVTSLNSSAT
				AGCGCATCTTTGACCTACAGAACAAGGTTCT		GRCLKIYRTFRDEEGKEYVRC
				GTCATCAACTGAAGTCTTATCAACTGACACAG		ETVRKPAVIDAYVRIRTTKDEE
				ACAGCAGCTCAGCTGAAGATAGTGACTTTGA		FIRKFALFDEQHREEMRKERR
				AGAAATGGGAAAGAACATTGAGAACATGTTG		RIQEQLRRLKRNQEKEKLKGP
				CAGAACAAGAAACCAGCTCTCAGCTTTCAC		PEKKPKKMKERPDLKLKCGAC
				GTGAACGGGAGGAACAGGAGCGGAAGGAAC		GAIGHMRTNKFCPLYYQTNAP
				TACAGCGAATGCTACTGGCAGCAGGCTCAGC		PSNPVAMTEEQEEELEKTVIH
				AGCATCCGGAAACAATCACAGAGATGATGAC		NDNEELIKVEGTKIVLGKQLIES
_				ACAGCTTCCGTGACTAGCCTTAACTCTTCTGC		ADEVRRKSLVLKFPKQQLPPK
				CACTGGACGCTGTCTCAAGATTTATCGCACG		KKRRVGTTVHCDYLNRPHKSI
				TTTCGAGATGAAGAGGGGAAAGAGTATGTTC		HRRRTDPMVTLSSILESIINDM
				GCTGTGAGACAGTCCGAAAACCAGCTGTCAT		RDLPNTYPFHTPVNAKVVKDY
				TGATGCCTATGTGCGCATACGGACTACAAAA		YKIITRPMDLQTLRENVRKRLY
				GATGAGGAATTCATTCGAAAATTTGCCCTTTT		PSREEFREHLELIVKNSATYN
				TGATGAACAACATCGGGAAGAGATGCGAAAA		GPKHSLTQISQSMLDLCDEKL
				GAACGGCGGAGGATTCAAGAGCAACTGAGG		KEKEDKLARLEKAINPLLDDDD
				CGGCTTAAGAGGAACCAGGAAAAGGAGAAG		QVAFSFILDNIVTQKMMAVPD
				CTTAAGGGTCCTCCTGAGAAGAAGCCCAAGA		SWPFHHPVNKKFVPDYYKVIV
				AAATGAAGGAGCGTCCTGACCTAAAACTGAA		NPMDLETIRKNISKHKYQSRE
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		GATGGTGATCTTGCAGATGAAGAGGAAGGAA	

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	PLYSTRLILTSPLAYL*LFSLRV RPQLSLSTTYLSIYYTCSFKITE KQIYYLEYCVNIQFSLVLQYPV KRLSSKIA*VSSFSMQLFQ*GXI MRL*YC*	PPHLTLVFF*RGPLLLSLRLMIA KTTKDTIVTGQPWNLVLGNGG L*FVTHKKRLKGPKCR*ESLVIE QTRTGDQCQ*FVMNVLGFLC DQPVGISV
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AGCATCGCAGGGCTCAGGACCAACCGCATA G	GTGGGAACAAGACTATACAATAACTTTGTGGGAACAAGAGGGATATTTTCATACTTTTTTTCATACTTTTTTTT
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AGACAGCAACA GCCAGTCAGA AATCACCCATG CAGTGCTCAAC	GAAGAAAGAC GCGAGCAGCT ACATGCTTGGC GGAATCCCATG CTACAGCCTG	CIGIOCGAGA CACACATCAAC CCCTGCCCC TCCCTTGACO CATCTATGCAC TGACACACAG ACTCACCGCA GGCAGTCCAC	CTTTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	AGTGGTATAT AACCTATGT TGGTGATCGA TCTTCCCACT ACTTCAAGTT AGTGAAGATC

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			TGCGAGGGAGACTCTGGCTTCTCTCTCAGA TGCGGTGACGGATCTTGCCTCACACCCTGGT TACTACGGGAATCTGGTGGAGGAGTCCCTGG	TTKQNVLRVVIPEVSILPEDLE ELYDLFKREHMMSCYWEQPR PMASRHDPSRPYAEQYRIDAR

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GATGGCCAGGCCTTGATGATCGTCAGCAGGT TTCTAGATCACATTAAGAATGAGGACAGCCC AGGGCCCCCAGTTGGCACCCTGTGA TTCTCCGACGACCCTGCTGTAT GAGAATTTCGGACCTGTTCCTAT GAGAATTTCGGACCTGTTCCTAT GAGAACTTCGGAGCCTGTTCCTAA GCGACCTACCTTATCCCGGAA GCTCCAATTCTCCTGAAGGACCCAAA GCTCAATTCTTCCTGAAGACCTATTATCCCGGAA GCTCCAATTCTTCCTGAAGACCTATGATGA GCTCAACTTATTCAAGAGCCCATG GCTCAACTTCTTCAAGACCCTAT GCCTCACGCCCTTTCAGAGGCCCTAT GCTCAACTTCTTCAGGAGCCCTAT GCTCAAGGCCCCACCGCCCTAT GCTCAAGGCCCCACCAGCCCCTAT GCTCAAGGACCTTTCAGCTGCCCGCCCT GGCCCACGCCCCACCGCCCCTT GCTCAAGGACCTTCAGCTCCGCCTT GGACCTGCGGGCCCCACAGGCCCCT GGACCTGCGGCCCCACAGGCCCCTT GGACCTGCGGGCCCCACAGGCAGC CCGAAAGGACGTTCAGGTTCAAAGCGTTT GCACCACTTCAGGCTTCCGCCTTT GGACCTGCGGGCCCCACAGGAGTCCTCG CCGAAAGGACGTTCAGGTTCAAAGCGTTT GTGACCTGCCCATTTATGTATATGTAATGGAG	CAATGCTGAGGACCTGTGCAGCAGGAT	
TTCTAGATCACATTAAGAATGAGGACGCC AGGCCCCAGTTGCCATGCCTTT TTCTCCGACGACCAGCTCCGGGATTCCTAT CTGATATTTCGGAGCCTGATCCTAT GAGAATTTGGGACCTGATCGTAT GAGAATTTGGGACCTGATCCGGATCCTAT GAGAATTTGGAGCCGAGGATCAAA TCGAGCACCTACGTTACAAGCACAAA GCAGAACGTTCCTCGAGGACCAAA GCAGAACGTTCTCCAAAGCACAAA GCTGATCTTCCTGAGCCCAGGCCAAA GCTGATTCTTCCTGAGCCCAGCCC	GATGGCCAGGCCTTGATGATCCTCAGCAGGT	
AGGCCCCCAGTTGGCATGCCTTT TTCTCCGACGACGAGCCCTACCTGTGA CTGATATTTCGGACCTGATCCGGGATTCTAT GAGAATTTGGAGCCAGTTGTGGAGCAGA TCGAGCACCTACGTTACAGCAGGATCAG GATCTTCCAGGCCCACGAGGACCAAA GCTCACAGTTTCTCCTGAAGACCTAGAGAGC TCTACGACTTATTCAGAGACCTAGAGAG GCTTACGACTTATTCAGAGCCCAGC TCTACGACTTATTCAGAGCCCAGC GCTGAGCAGTTATTCAGGCCCATAGAG GCTGAGCAGTTATTCAGCGGCCCATA GCTGAGCAGTTACTGGGACCCCAGCCGGCCCATA GCTGAGCAGTTCAGGCCCACGCCCCTAT GCTGAGCAGTTCAGGCCCACGCCCCAGC TTTGCACACCTGTTTCAGCTAGTCTCCCC GCAAAGGACCTTTCAGGCCCACAGCCCGCAG GCTGAGCCCTCTTCAGGCTTTCAGCTTTCAGCTTTCTCGCAGATCCTCG GCTGAGCCTCCCACCACCCCCTTTTCAGCTTTCTCTCGCAGATCCTCG GCTGAGCCTCCCACCACCCCCTTTTCAGCTTTCTCTCTCT	TTCTAGATCACATTAAGAATGAGGACAGCCC	
TTCTCCGACGAGCCCTACCCTGTGA CTGATATTTCGGAGCCTGATCCGGGATTCCTAT GAGAAATTTGGAGCCTGATCCGGGATCCTAT GAGAAATTTGGAGCCAGGGACCAGAG TCGAGCACCTACGTTACCAGGACCACAAA GGTCCTCCAGGCCCACGAGGACCACAAA GCTCCAATTCTTCCTGAGGACCATATG AGCTGTTACTGGGAGCACCATATG GCTGAGCCTCACGCCCAGCCCGGCCATA GCTGAGCGCCACCAGCCCGGCCAG GCTGAGCGCCCACGCCCAGCCCGCCAG GCTGAGCGCCCACACCCCTAT GCTGAGCCTTCTTCAGGTTTCAGCTAGTCTCGCCC GCTGAGCGCCCACACCCCAGCCCCCTAT GCTGAGCCTCCCGCATAGACGCCCCTAT GCTGAGCCTCCACGCCCCCTTTCCCGCCCTCCGCCCCTTTCCGGCCCCCTTTCCGCCCCCTTTCCGCCCCCTTTCCGCCCCTTTCCGCCCCTTTCCGCCCCTTTCCGCCCCTTTCCGCCCCTTTCCGCCCCCTTTCCGCCCCTTTCCGCCTTTCCGCCTTTTCCTCGCTTTCCGCCTTTTCCTCGCTTTTCCTTCGCTTTTCCTTCCGCTTTTCCTTCCGCTTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCTTTT	AGGGCCCCAGTTGGCAGCCACCATGCCTTT	
CTGATATTTCGGACCTGATCCGGGATTCCTAT GAGAATTTGGAGCCAGTCTGTGGAGCAGA TCGAGCACCTACGTTACAAGCACAGA TCGAGCACCTACGTTACAAGCACAAA GCTCTCCAAGGCCACGAGAACATCGTACAAA GTCTCAATTCTTCCTGAAGACATTGATG AGCTGTTACTGGAGCAGCCCATG GCCTCACGCCCACGACCCATG GCCTCACGCCCACGACCCATG GCCTCACGCCCACGACCCATG GCTGAGCACTTTTCAAGACATTCTCGCAGCCCATG GCTGAGCACTTTTCAAGACATTCTCGCCATG GCTGAGCACTTTTCAAGACATTCTCGCCATG GCTGAGCACGCCCACGCCCGCTAT GCTGAGCACCTGTTTCAAGAGATCCTCG CCGAAAGGACCTTCAGGTTCAAGCGTTTTCAAGCTTCTTTCAAGCTTCTTTCAAGATTCTTCGATTTTTTTT	TTCTCCGACGACCAGGAGCCCTACCCTGTGA	
GAGAAATTTGGAGACCAGTCTGTGGAGCAGA TCGAGCACCTACGTTACAAGCACAGAAA GGTCCTCCAAGGCCACGAGGACCACAAA GCAGAACGTCCTCGAGTCGTTATCCCGGAA GTCTCAATTCTTCCTGAAGACCTAGAGC TCTACGACTTATTCAAGAGACATG AGCTGTTACTGGAGCCCAGGCCCATG GCTCACGCCCACGCCCGGCCCTAT GCTGAGCAGTACCGCATAGACCTTAT GCTGAGCACTTTTCAGCTAGTCTCGCCCT TTGCACACCTGTTTCAGCTAGTCTCGCCCT GGAAAGGACCTTCGGAGCCCCTCG CCGAAAGGACCTCAGGCCCACAGGCCCTCG CCGAAAGGACCTCAGGTTCAAGACCTTTTCAGCTTCTCGCCTTCGCCTTCGCCTTCGGGGCCCCACACGGAGATCCTCG CCGAAAGGACCTCATCAGATTTATGATAATGGAGCTTTTAATGTATAATGGAG	CTGATATTTCGGACCTGATCCGGGATTCCTAT	
TCGAGCACCTACGTTACAAGGATCAGA GGTCCTCCAAGGCCACGAGGACCACAAA GCAGAACGTGCTTCCGGAGGAGC GTCTCAATTCTTCCTGAAGAGAGCTG TCTACGACTTATTCAAGAGACCATG AGCTGTTACTGGGAGCCCCAGGCCCATG GCCTCACGCCACCCCAGCCCGGCCCTAT GCTGAGCAGTACTCGCATAGTCTCCC GGACCTGCGGCCCCAGGCCCCTA GGACCTGCGGGCCCCAGGCCCCTA GGACCTGCGGGCCCCAGGCCCCT GGACCTGCGGGCCCCCTCTCGCCC GGACCTGCGGGCCCCCTCTCGCCCT GGACCTGCGGGCCCCCCTCTCGCCCCTCC GGACCTGCGGGCCCCCCTCTCGCCCTCC GGACCTGCGGGCCCCCCCTCCTCCC GGACCTCCGGCCCCCCTTGGATCCTCCG CCTGGACCTCCTCGATATATGTATATGTATATGGACAA	 GAGAAATTTGGAGACCAGTCTGTGGAGCAGA	
GGTCCTCCAAGGCCACAAA GCAGAACGTCCTTCGAGTCGTTATCCCGGAA GTCTCAATTCTTCCTGAAGACCTAGAGGAGC TCTACGACTTATTCAAGAGAACATATGATG AGCTGTTACTGGGAGCACCCAGCCCATG GCTCACGCCACGACCCCAGCCCGCCAT GCTCACGCCACGACCCCAGCCCCTAT GCTCACGCCACGACCCCAGCCCGCCAG CCGAAGGACCTTTCAGCTTTCAGCTCTCGCCCT GGACCTGCCGGGCCCCACAGCCCT GGACCTGCCGGCCCCTTTCAGCTTTCAGCTTCAGCTCTCG GGACCTGCCGGGCCCCACAGGCCTTCGGATCCTCG GGACCTGCCGGCCCCTTTGGATGACGCTTT CCGAAGGACCTTCAGCCTTTTATGTATAATGGAG GTGAGCTGCCTCCGATATTATGTATAATGGAG	TCGAGCACCTACGTTACAAGCACAGGATCAG	
GCAGAACGTGCTTCGGAGACCGGAA GTCTCAATTCTTCCTGAAGACCTAGAGGAGC TCTACGACTTATTCAAGAGACCATGATG AGCTGTTACTGGGAGCACCCAGGCCCATG GCTCACGCCCACGACCCGGCCCTAT GCTGAGCACTACGCATAGACGCCCTAT GCTGAGCACCTGTTTCAGCTAGTCTCGCCT GGACCTGCGGGCCCCACGAGATCCTCG GGACCTGCGGGGCCCATAGACGCTT GGACCTGCGGGCCCCACGAGATCCTCG GGACCTGCGGGCCCCACAGAGCCTTT GGACCTGCGGGCCCCATAGATGGAG CCGAAAGGACCTTCAGGCTTTATGTATAATGGAG	 GGTCCTCCAAGGCCACGAGGACACCACAAA	
GTCTCAATTCTTCCTGAAGACCTAGAGGGGGC TCTACGACTTATTCAAGAGAACATATGATG AGCTGTTACTGGGAGCCCCAGGCCCATG GCCTCACGCCACGACCCCAGCCCGTT GCTGAGCAGTACCGCATAGACGCCCTAT GCTGAGCAGTACCGCCATAGACGCCCT CGGAAGGACCTTTCAGCTTTCGCTC GGACCTGCGGGCCCCACAGGAGATCCTCG CCGAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCACCTCATCGATTATGTATAATGGAG	GCAGAACGTGCTTCGAGTCGTTATCCCGGAA	
TCTACGACTTATTCAAGAGAGACATATGATG AGCTGTTACTGGGAGCCCCAGGCCCATG GCCTCACGCCACGACCCCGGCCCTAT GCTGAGCAGTACCGCATAGACGCCCGGCAG TTTGCACACCTGTTTCAGCTAGTCTCGCCT GGACCTGCGGGGCCCACAGAGATCCTCG CCGAAAGGACGTTCAGGTTCAGATGATGAAAGCGTTT CATGGACCACCTCATCGAGTTCAAGCGTTT GTGAGCTCCTCGATATTATGTATAATGGAG	GTCTCAATTCTTCCTGAAGACCTAGAGGAGC	
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GCCTCACGCCACGACCGGCCTAT GCTGAGCAGTACCGCATAGACGCCGGCAG TTTGCACACCTGTTTCAGCTAGTCTCGCCT GGACCTGCGGGGCCCACACGGAGATCCTCG CCGAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCACCGCTTCAGGTTCAAGCGTTT GTGAGCTCCTCGATTAATGGAG	AGCTGTTACTGGGAGCAGCCCAGGCCCATG	
GCTGAGCAGTACCGCCGGCAG TTTGCACACCTGTTTCAGCTAGTCTCGCCCT GGACCTGCGGGGCCCACAGGGAATCCTCG CCGAAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCACTCCACCAGGTTCAAAGCGTTT GTGAGCTCCTCGATTAATGGAG	GCCTCACGCCACGACCCCAGCCGGCCCTAT	
TTTGCACCCTGTTTCAGCTAGTCTCGCCCT GGACCTGCGGGGCCCACACGGAGATCCTCG CCGAAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCAGCTCATCGAGTTCAAAGCGTTT GTGAGCTGCTCATCGAGTTTAATGGAG	 GCTGAGCAGTACCGCATAGACGCCCGGCAG	
GGACCTGCGGGGCCCACAGGAGATCCTCG CCGAAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCAGCTCATCGAGTTCAAAGCGTTT GTGAGCTGCCTCGATATTATGTATAATGGAG	TTTGCACACCTGTTTCAGCTAGTCTCGCCCT	
CCGAAAGGACGTTCAGGCTCTTGGATGACAA CATGGACCAGCTCATCGAGTTCAAAGCGTTT GTGAGCTGCCTCGATATTATGTATAATGGAG	GGACCTGCGGGGCCCACGGGAGATCCTCG	
CATGGACCAGCTCATCGAGTTCAAAGCGTTT GTGAGCTGCCTCGATATTATGTATAATGGAG	CCGAAAGGACGTTCAGGCTCTTGGATGACAA	
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GAAACAGCTGAAGCAGATTAAGGATTTA GCCAAAGAAAAGGAATTTATCCAG GCCAAAATGAGCCAGAGGAATTTATCCAG TTCTGTAAAACTCTGTACAGTATTATCCAGA AGATCCAGAAGAAAATGATTTATATCCAGCA TCGCCACACTCACCACACTGCTGCTGCTGCTGCTGCTGCTGCAGCT CTGGAAGCTCACCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC				GGAAACCCAATGGTGATGCAGTTGATTATCA	
GCCAAAATGACTGAGAAATTATCCAG TTCTGTAAAATGAGTTTTTTTCCAGA AGATCCAGAGAAATGAGTTTTGTACAGGT TCGCCACACTCTACAGTTTTGTACAGGT TCGCCACACTCTACAGTTTGTACAGGT TCGCCACAGTCACACTGCTGCTGCTGCAGT TCGCCACAGTCACACTGCTGCTGCTGCAGT TCGCACAGTCACCACTGCTGCTGCAGT TCGCAAGTTTTTGCAGAGCTGCTCTTGAGGT TTTTGCTTTTTTGCAGCACTTTTTCTGAGGCGCA GAGGGCTTTTTTGCAGCTCCTTTGAGCTCATTA ATTCAGATTTTTTGAAAAGCCACTGGAACTATA GTCAACTTTTTTGAAAATGCCAAGTCATTA ATCCAACTTTGAACTTTGAACTTGAACTTGAA ATCCAACTTTGAACTTCATAATGAGCCACTGAT ACCAACTTTGAACTTTTGAACTTGAACTTGAA ATCCCAACTTTGAACTTGAACTTGAA ATCCCAACTTTGAACTTGAACTTGAA ATCCCAACTTTGAACTTGAACTTGAA ATCCCAACTTTGAACTTGAACTTGAA ATCCCAACTTTGAACTTTTTGAACTTGAA ATCTCCAGACTTTTTGAACTTGAACTTGAA ATCCCAACTTTTAAATGGCTGAGTGGCCC AGGCCTCTTTTTTGAACTTGAACTTGAA ATCTCCAGACTTTTTAAATGGCTGAGTGGCCC AGGCCTCTTTTTAAATGGCTGAATTGTGCC AGGCCTCTTTTTAATGAAATTGTCAATTTAAGTGCCAGG ACGCCACTGGCTGCTTTTAATGAAATTGTCAATTTAATGAAATTGTCAATTGAA ATCGGGACTTCCAGGACCCCTATTGAA ATCGGGACTTCCAGGCTTTTAATGAAATTGTCAATTTAATGAAATTGTCAATTGTGA ATCGGGACTTCCAGGCTTCCATTGAT AGGCATCTCCAGGACCCCTATTGAA ATCGGGACTTCCAGGACCCCTATTGAT AGGCATCTCCAGGACCCCTATTGAT AGGCACCCATGAAAGTTTCCAGGACTCTTTAATGAAATTGTCATCTTCCATGGA ATCGGGACCCCAGGCTTCCAGGACTCTTTAATGAAATTGTCATCTTCCATGGA ATCGGGACCCCAGGCTTCCAGGACTCTTTAATGAAATTGTCATCTTCCATGGA ATCGGGACCCAGGCCCACGGCTTTAATGAAGTGTGAA ATCGGGACCCCAGGCCCACGGCTTTAATGAAGGACTCCTTGAAATTGTCATCTTCCATGGAAATTGTTCATCTTCCATGGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAATTGTTCAATGTGAAAATTGTTCAATGTGAAAATTGTTCAATGTGAAAATTGTTCAATGTGAAAATTGTTCAAAAGAATTGTTCAAAAGAATTGTTCAAAGAAATTGTTCAAAAGAAATTGTTCAAAAATTGTTCAAAAGAAATTGTTCAAAAATTGTTCAAAAATTGTTCAAAAATTGTTCAAAAATTGTTCAAAAAAAA	-			GAAACAGCTGAAGCAGATGATTAAGGATTTA	
GCCCAAATGAGGCCGGGAATTTATCCAGA TTCTGTAAAACTCTGTACAGTATGTTCCATGA AGATCCAGAACAAATGATTTGTACAGCCA TCGCCACAGTCACCACTGCTGCTGCAGAT TCGCCACAGTCACCACTGCTGCTGCAGT CGGGAGGTGGGGCAGCAGCTGCTGCAGCT CTGGAAGCTGCTCCCAGGAGTGGGGAGG AGCTGCGGGCTTTTGCAGACTCTTCTCCTGAGGA CTCGGTTTTTGCAGACTCCTTCCAGAGGCGCC CAGGACTCCCAGGCACTTCCAGAGGCGCC CAGGACTCCCAGGCACTTCCAGAGGCGCC CAGGACTCCCAGGCACTTCCAGAGGCGCC CAGGACTCCCAGGCACTTCCAGAGCGCCC CAGGACTCCCAGGCACTTCAACATTA ATCCAACTTTTTAAAAGCTCAACATTAA ATCCAACTTTTTAAAATTCCAAGATTAAA TCACAACTTTTAAAATTTTGAAATGCAACTTGAA ATCCCAACTTTTTAAAATTTTGAAACTTGTA CAGCCACCCTACAGGTACTTTT CACAATCTCAAACTTTTAAATGCTGAGTACTTGTA CAGCCACCCTACAGGTACTTTTT CAGATCTCCAGAACTTTTTTTTAA CAGCCACCCTACAGGTACTTTTT CAGCACTTTTTTAAATTTTTAAATTTTAATGAATTGCAGCCCC CAGCCACTGCTGCATTTTTAATGAATTGCAGCTGCTTTTAATGAAATTGTCATCTTTTAATGAA CACTTTAATGAAATTGTCATCTTTAATGAA CACTTAATTGAAATTGTCATCTTTTAATGAA CACTTGCGGACCTCGGTTTTAATGAAATTGTCATCTTTAATGAA TGGACACCATGTAAATGGCTTAATTGAAA TGGACACCCAGGCCCCAGGCTTCCATGAA ATCGGGACCCCAGGCTTCCATGAA TGGACACCCAGGCTTCAATGTGAA TGGACACCCATGAAATTGTCATCTCTTAATGAA TGGACACCCAGGCTCCATGAAGAATACTGGA ATCGGGACCCAGGCTTCCATGGA ATCGGGACCCCAGGCTTCATTCCAGCTGTTCCAGTGGA ATCGGGACCCAGGCTTCATCTCCTTGAA TGGACACCTGCAGAGTATTCATGTTCATCTCCTTAATGAA TGGACACCAGGCTCCAGGCTTCATGAA TGGACACCTGGCTTCAAGTGTGAA TGGACACCTGCTAAACGGCTCCAGGCTTTAATTGAAATTGTCATCTTCCAGTGGAA TGGACACCCAGGCCCAGGCTTCAAGTGTGAA TGGACACCCAGGCCCAGGCTTCAAGTGTAAAGGAACCCAGCTTCAACTGCAAGATAATGTGAA TGGACACCCAGGCCCAGGCCCAGGCCCACGCCAGGCTCCAAGATAATCGTCAACTGAACCCAACACTGCAACACTGTAAAAGGAACCCAACACTACTAAAAGAATTCTCAACTGCAACCTTCAACTGCAACTACTAAAGAATCTTCAACTGCAACACTACTAAAAGAATCATCAACTACTAAAGAACCCAACACTACTAAAAGAATCATCTCAACTGCAACACTACTAAACACACAC				GCCAAAGAAAAAGATAAAACTGAGAAAGAATT	
TICTGTAAAACTCTGTACAGTATGTTCCATGA AGATCCAGAAGAAATGATTTGTATCAAGCCA TCGCCACAGTCACCAGCACGCGCAGCAGCAGC CGGGGAGGTGGGGCACCCCAGGAGCAGCAGC CGGGAGGTTCGGGCACGCAGCAGCAGCAGC CGGGACTCCCAGGACTCTCTCTCTGAGC CAGGACTCCCAGGACTCCCAGGAGCCGCC CAGGACTCCCAGGACTCCCATCTCTGAACATA TITTAGCTTCACTTCTGACTGAACATA TTTAGCTTCACTTCTGACTGAACATA TCCAAACTTTTTGAAAAGCCACTGGAAGCCCC CAGGACTCCAAACTTTTTGAAAATGCCAAGATCATA TCACAACTTCTAAAATGCCAAGATCATTA TCACAACTTTTTTGAAAATGCCAAGATCATTA TCACAACTTCAAAATTGCAACATTGTA TCACAACTTTTTTGAAATGCCAGGACCCTCGCAACTTA TCACAACTTCAAACTTTTTTTTTT				GCCCAAAATGAGCCAGAGAATTTATCCAG	
AGATCCAGAAAATGATTTGTATCAAGCCA TCGCCACAGTCACCACTGCTGCTGCAGAT CGGGAGGTGGGGCACCACTGCTGCTGCAGAT CGGGAGGTGGGGCACCACTGCTGCAGCACT CTGGAAGCTGCTCCCAGGAGTGTGGGAGG CTGGATTTTGCAGACCTTCCCTGAGGA CTGGGTTTTGCAGACACTTCCAGAGACCCC CAGGACTCCCAGGCACTTCCAGAGACATA TTTTAGCTTCCATTTTGAACACATA TTTTAGCTTCAAACTTTTGAACAGTCATA GTCAAACTTTTTGAAAATGCACTGGACATGA ATCCAAACTTGAACTTTTGAACAGTCATCAGT ACAATCTCAAACTTTAGAATGAACTTGTA TCACAATCTGAACTTTTGAATGAGCCACTGGA TCACAATCTGAACTTTTGAACTTTTGGAGCTCAT GCCAATCTCAAACTTTAGAGTCAATCAT ACAGCCTCTTGCACTGGTACTTGTA CAGCCACTGGACCTTTTTGGAACTTTTGGAGCTCA GGCCACTGGCTCCTTTTTGGAGCTCAT GGCCACTGGCTCCTTTTTTGGAGCTCAC GGCCACTGGCTCCTTTTTTGGAGCTCAG GGCCACTGGCTCTTTTTTTTTT				TTCTGTAAAACTCTGTACAGTATGTTCCATGA	
TCGCCACAGTCACCACTGCTGCTGCAGGAT CGGGGAGGTGGGCCAGCAGCAGCAGC CTGGAGCTGCTCCCAGGAGTGTGGGGAGG AGCTGCGGGCTTCAGCTCTCTCTGAGGA CTCGGTTTTTGCAGACACTTCCAGAGGCCGC CAGGACTCCCAGGACTTCCAGAGGCCGC CAGGACTTCTCAGTTCTCCAGAGCCCC CAGGACTTCTCACTTCTCCAGAGCCCC CAGGACTTCTTTTGAAATGCACTTAA ATCCAAACTTCAAAATGCCAGACATTAA ATCCAAACTTCAAAATGCCAGACTTGAA ACCAATCTCAAAATGCCAGACTTGAA TCACAATCTCAAAATGCCAGATCATGTA CACAATCTCAAAATGCCAGACTTGAA TCACAATCTGAAATGCCAGACTTGTA G TCTCCCAGACCTTCACTGCAGTCATCTC GCCCACTTCTTGCATCTTTTGCAGTCGTCCT GGCCACCTTCTTGCATCTTTTGGAGCTCC AGGCATCGAGGCTTTTTGCAGTGGTCGCT GGCCACTGGCTGTTTTAGAAGCGCCC AGGCATCTTATATGAAATTGTCATCTTTACGTCAGA GCCTTTATATGAAATTGTCATCTTTACGTCAGA TGGACACCTGGCTTCCATGAT AGTGTGGACCCCATGGCTTCATTTACTGAA TGGACACCATGCCTTGTTCCACTCATTGAT AGTGTGGACCCCATGGCTTCATTTACTGAA TGGACACCATGCCTTGTTCCACTCATTGAT AGTGTGGACCCCATGGCTTTCATTTACTGAA TCGGGACCCCATGGCTTCATTTACTGAA TGGACACCATGACTTTAAAGGATTACTATTACTGAA TGGACACCATGCCATG				AGATCCAGAAGAAAATGATTTGTATCAAGCCA	
CGGGAGCTGCGGAGCAGCAGCAGCAGCAGCAGCTCTGCTGCAGGAGCAGCAGCTCCCAGGAGTGTGGGGAGGAGCTGCAGCAGCTCCCTTCTCCTGAGGAGAGCTGCTCCCTTCTCCTGAGGAGAGCTGCTCCCTTCTCCTGAGGAGCCCCCCAGGACTCCCAGGAGCCCCCCCC				TCGCCACAGTCACCACACTGCTGCTGCAGAT	
CTGGAAGCTGCCCAGGAGTGTGGGAGGAGAGAGGAGAGAGCTGCGGGACTTCTCCTGAGGAAGCTGCTTCTCCTGAGGAAGCTGCTTCTCCTGAGGAAGGA				CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
AGCTGCGGCTTCAGCTCCTCCTGAGGA CTCGGTTTTGCAGACTCCGGAAGACGCC CAGGACTCCCAGGCACTTCCAGAGGCGCC CAGGACTCCCAGGCACTTCCAGAGGCGCATA TTTTAGCTTCACTTCTGCACTGAACATA TTTTAGCTTCACTTCTGACTGAACATGAACATA GTCAAACTTTTTGAAAAGCCACTGGACAGGACA				CTGGAAGCTGCTCCCAGGAGTGTGGGGGAGG	
CTCGGTTTTTGCAGACCTGGGAAGACGCCC CAGGACTCCCAGGCACTTCCAGAGGCGCA GAAAGGGACTCCCAGGCACTTCCAGAGGCGCA TTTTAGCTTCACTTCTGACTGAACATA TTTTAGCTTCTACTTCTGACTGAACATGAA ATCCAAACTTGAAATGCCAAGATCAGT ACAATCTCAAAACTTTGAAATGACACTGAA TCCAAACTTGAAATGCCAGGACCACTGAA TCCAAACTTGAAATGCCAAGATCAGT ACAATCTCAAAACTTTGAAATGAATGAA TCCAAACTTTAGAAATGCCAACTGAA TCCCAAACTTGAACTTGAATCAGTACTAC GCCCACTGCTCTTGCATCTTTGCACTCACTCAC GCCCACTGGCTGGCTGGCTCACAGA CCGCCACTGGCTGGCTCATTAGAAGCGCCC AGCCATCGCAGACCTTTTAAGAAGCGCCC AGCCATCGCATGATCTTTAAGAAGCGCCC AGCCATCGCATGATCATCATTCAACAGA GCCATTCCAGGACCCTCATTGAT AGCCATCGCATGATTCCACTCATTGAT AGCCATCCACTGACTCATTCATTGAA TGGACACCAGGACCCACAAGATACTGGA TGGACACCAGGACCCACAAGATACTTGAA TCGGGACCCACAGATATTCATGAAATGCTGAA TCCGGACCCACAGATATTCATGAAATACTGAA TCCGGACCCCACACACACATACTGAA TCCGGACCCCACACACACATACTGAA TCCGGACCCCACACACACATACTGAA TCCGGACCCCACACACACTACTATTCATTCATTCATTTCATTTCATTTCATTTCATTTCATTTCATTTCATTTTTCATTTTTT				AGCTGCGGGCTTCAGCTCCTTCTCCTGAGGA	
CAGGACTCCCAGGCACTTCCAGAGGCGGCA GAAAGGGACTGGACT				CTCGGTTTTTGCAGACACTGGGAAGACGCCC	
GAAAGGGACTGGACTGCCTTGAACATA TITTAGCTTCACTTCTGACTGAACAGTCATTA GTCAACTTTTTGAAAAGCCACTGGACATGAA ATCCAACTTGAAAATGCCAAGATCAATCAGT ACAATCTCAAAATGCCAAGATCAATCAGT ACAATCTCAAAATGCCAAGATCAATCAGT ACAATCTCAAAACTTTTGAAATGAGCCACCAA TCACAATCTGAACTTTTGAATTGAA	-			CAGGACTCCCAGGCACTTCCAGAGGCGGCA	
TITTAGCTTCACTTCTGACTGACAGTCATTA GTCAACTTTTTGAAAAGCCACTGGACATGAA ATCCAAACTTGAAAATGCCAAGATCAGT ACAATCTCAAAACTTTTGAAATGAGCCACCAA TCACAATCTGAAACTTTTGAAATGAGCCACCAA TCACAATCTGAACTTTTGAAATGAGCCACCACAA TCACAATCTGAACTTTTGAATGAGCTGAC GCCACTCTGCACCGTTTTGGAGCTCA CCGCCCTCTTGCATCTTTTTTTGAGCTGC CCGCCCTCTTTTTAGAGAGCCCC AGGCATCGAGCTTTTAAGAAGCGCCC AGGCATCGAGATTGTCATCTTTACGTCAGA GCCTTTATATGAAATTGTCATCTTTACGTCAGA GACTGGCATGACTGGCTTCATCTTTACGTCAGA GCCTATTCCGGGACCCCAGGTTCCATGGA TGGACACCATGTAAAGGATATTTCATGTGTGAA ATCGGGACCCAGGTCGAGTAGTTTTCATGTGTGAA ATCGGGACCCAGGTCGAGTAGTTTTTCATGTGTGAA ATCGGGACCCAGGTCGAGTAGTTTTTTTTTT				GAAAGGGACTGGCTGTCCCCTTGAACATA	
GTCAACTTTTTGAAAAGCCACTGGACATGAA ATCCAAACTTGAAAATGCCAAGATCAGT ACATCTCAAAATGCCAAGATCAGT ACATCTCAAAACTTTGAAATGAGCCACCAA TCACAATCTGAACTTTGAAATGAGCACACACAA TCACAATCTGAACTTTGAAATGACTTGTA G CAGCCACTGCACCCTCTGCAGTGCTACAC CAGCCACTGCTCTTTTTTTTTT				TTTTAGCTTCACTTCTGACTGAACAGTCATTA	
ATCCAAACTTGAAAATGCCAAGATCAGT ACAATCTCAAAACTTTGAAATGAGCCACCAA TCACAATCTCAAAACTTAAGCTGAGTAACTTGTA G TCACCAATCTGAACTTAAGCTGAGTAACTTGTA G TCTCCCAGACCTCTGCAGGAACCGTACTAC CAGCCACCCTCTGCACTGTTTGGAGCTCA CCGCGCTCCTTTTTTTTTT				GTCAACTTTTTGAAAAGCCACTGGACATGAA	
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	CTGTTTGACCTGAAAGTGGGTATGGAACAGC	HAFLLYLGYTPQAAREVRIMQ
	TGGTACAGAATGCCACCTTCCGCTGCATCCT	FCHTLREFALEYRTCRERVLQ
	 GGCTACCCTCCTAGCTGTGGGCAACTTCCTC	QQQKQATYRERNKTRGRMIT
	 AATGGCTCCCAGAGCAGCGGCTTTGAGCTGA	ETEKFSGVAGEAPSNPSVPVA
	 GCTACCTGGAGGAGGTGTCAGATGTGAAGGA	VSSGPGRGDADSHASMKSLL
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	 CTCTGCTCCCTAGTGCTCCAGACCCGGCCTG	SPIMPTVGPSTASPEEPPGSS
	AGTCCTCTGACCTCTATTCAGAAATCCCTGCC	LPSDTSDEIMDLLVQSVTKSSP
	CTGACCCGCTGTGCCAAGGTGGACTTTGAAC	RALAARERKRSRGNRKSLRR
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	 GGAGCTTGGCCAAGCATGAGCTGGCCCCAG	
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Shigella ospC1	ო	prey2108	8	GCAGGAAGCTCAGAGTATCGATGAAATCTAC AAATACGACAAGAACAGCAAGAAATCC TGCCGCCAAGCCCTGGACTAAGGATCCC ATTACTTTAAGTACTGCAAAATCTCAGCATTG GCTGCTGAAGATGGTGATGCATGCCAGAT CGGGAGGCAACTTGGATGGTGATGGCTCTGAT GCTGCTGAAGACTTGGATGGTGATGGTGATC ATTATGGAAGTTTTGCTTTGC	QEAQSIDEIYKYDKKQQGEILA AKPWTKDHHYFKYCKISALAL LKMVMHARSGGNLEVMGLML GKVDGETMIIMDSFALPVEGT ETRVNAQAAAYEYMAAYIENA KQVGRLENAIGWYHSHPGYG CWLSGIDVSTQMLNQQFQEP FVAVVIDPTRTISAGKVNLGAF RTYPKGYKPPDEGPSEYQTIP LNKIEDFGVHCKQYYALEVSY FKSSLDRKLLELLWNKYWVNT LSSSLLTNADYTTGQVFDLS EKLEQSEAQLGRGSFMLGLET HDRKSEDKLAKATRDSCKTTI EAIHGLMSQVIKDKLFNQINIS*

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Shigella ospC1	က	prey67403	93	TCTTGGCAGGAGCTTTGGATTTC ATGGCAATCAGATGGGGCAGAG CTGAGGGAATCAGAATGATCCT ACCTTTGATCTCTATTCTCTGCTA SCTTCCTCTATTCTCTGCTA STTCCATTTCCATGAATTTTCAT CAGGACAAAGGTTTTAGTCTTTG SAGACCTCTGACTTGGCTCTTGGAAAGGTTTTAGTCTTTGAAAGGTTTAGTCTTTG	294	LGHLGRSFGFL GNGNGMGG SVFC*GNQNDPSNSTFDLYSL LKMVLPLLPQTPVSVPFP*IFH QGHRTKVLVFGSNETSDLALD DYETSECICLFWNP
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				GTGAAACCATGATCATTATGGACAGTTTTGCT		LENAIGWYHSHPGYGCWLSG
				TTGCCTGTGGAGGGCACTGAAACCCGAGTAA		DVSTQMLNQQFQEPFVAVVID
				ATGCTCAGGCTGCTGCATATGAATACATGGC		PTRTISAGKVNLGAFRTYPKG
				TGCATACATAGAAAATGCAAAACAGGTTGGC		YKPPDEGPSEYQTIPLNKIEDF
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				GCCACCCTGGCTATGGCTGCTGGCTTTCTGG		KLLELLWNKYWVNTLSSSSLL
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				AGTTCCAGGAACCATTGTAGCAGTGGTGAT TGATCCAGGAACCATTTGTAGCAGTGGTGAT TGATCCAACAGAACAATATCCGCAGGGAAA GTGAATCTTGGCGCCTTTAGGACATACCCAA AGGGCTACAAACCTCCTGATGAAGGACCTTC TGAGTACCAGACTATTCCACTTAATAAAATAG AAGATTTTGGTGTACACTGCAAACATATTAT GCATCGCAAATTGCTTGAGCTGTTGTGGAAT AAATACTGGGTGAATACGTTGAGTTCTTCTAG AGGTCTTTGATTGCTGAAAAGTTCTGGC AGGTCTTTGATTGCTGAAAAGTTCTGGC AGGTCTTTGATTGCTGAAAAGTTCTGGC AGGTCTTTGATTGCCTGAAAAGTTCCAGGT AGGTCTTTGATTTGCCTGAAAAGTTCCAGGC AGGTCTTTGATTTGCCAAAAGTTCCAAAAT CAGAAGCCCAGCTGGCCAAAAT CAGAAGCCCAGCTGGGCAAAAT CAGAAGCCCAGCTGGGCAAAAT CAGAAGCCCAGCTGGGCAAAAT CAGAAGCTCTAAAAACTTGCCAAAGTAAACTG		DKLAKATRDSCKTTIEAIHGLM SQVIKDKLFNQINIS*	<u>Σ</u>
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TGGCCTCACTGAAAACCAGCTACAGCTCTCT	QAATSESSQSEASVKREESP MDVDOBSBSAODTOSIASDG
GTAGAGGTGTTGACATCCCACTCTTGT1CTG	TPOGEKEKEERPELPLLSEQ
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Dedi				TGCGGCTCCCCGCAGAGGTGGCACCACC		QGADPILATALASDPIPNPLQK
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				CGTTGCGCTGGAAGGAATTCGTGCGGCGCC		AALPPAPSLLR*
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<u> </u>				GACTCGGTGGACTTCTCGCTGGCCGACGCC		VELGELNDRFANYIDKVRFLE

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		GAGATGCGGGGGCGGCGGCAGGTGGAC	QHVQIDVDVSKPDLTAALRDV
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		ATGCGCCTCCGGGAGAATTGCAGGAGGAG	QESTEYRRQVQSLTCEVDALK
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				GGTCTCCTTGNTGTATCATGCCCTCGCTGGT		
				NTGGAGCCNNNGCGGGNCCTCTTGANTATG		
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				CGATCGCAACATCANATGCACGTATGTTNCTT		
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				CCAAATCAATACTACAAAATCCGCAGTCAAGC		PYPHKFHVDISI TDFIOKYSHI
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				ACTCACTGACTTCATCCAAAAATATAGTCACC		NSRNYKSEEEFIHINNKLRRG
				TGCAGCCTGGGGATCACCTGACTGACATCAC		DIIGVOGNPGKTKKGELSIIPYE
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Shigella ipaD	4	prey8889	105	GCTCAAGCCGGAGTTCATGCGGCGGCCGGA CAAGTCCTTCGACCCCTTCACTGAGGTCATC	306	LKPEFMRRPDKSFDPFTEVIV DGIVANALRVKVISGQFLSDRK
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				CAAGTACCGCACCCGGACCTCTCAGGGGAA		EANQPLCLPALLIYTEASDYIP
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				CCAGGACTATGCGGAGGCCCTGATCAACCC		DVEDTKEGEDEAKRYQEFQN
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				CAGGTGCCGCCTGCGGCCAGGTGCCCTAGG		
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307	MGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQ PYGPTFTTGDVIGCCVNLINNT CFYTKNGHSLGIAFTDLPPNLY PTVGLQTPGEVVDANFGQHP FVFDIEDYMREWRTKIQAQID RFPIGDREGEWQTMIQKMVS
Q.	GAGCCCAAGCTGCCCAGCTGGCCCAG GAGTGTCAGGAGCGCGCGAGGCTCCCC CAGGAGATCCGCCGGAGCCTGCTGGCCAGG ATGCCGGAGCCTGCTGGCCACC GGGAGCCTGTGGGCCTCTG GTGCCGTGTGCCACCACCGCCCC GGGAGCCACCTGTCGGCCCTCTG TCGCAGCACCTGTCGGCCCTCTC TCGCAGCACCTGTCGGCCCTCTC TCGAGATTGGTTTTCTGCTCAAGGTTGA ATGGGAATTGGTCTTTCTGCTCAAGGTTGA ATGGGAATTGGTCTTTCTGCTCAAGGTTTT CGTTTTGTTCTTCTGGAACTGGACATT CGTTTTGTTCTTCACTACTGGTGATGTCATTG GGACCAACTTTCACTACTGGTGATGTCATTG GGACCAACTTTCACTACTGGTGATGTCTTT CGTTTCACTGCCAACTTTACCACAGGTAT TGCTTTCACTGCCAACTTTACGGTAT TGCTTTCACTGCCAACTTTCGCCCAATTTGTATC CGTTTCACTGGCCAACTTTCCCCCCAATTTTCCCCTTCC CTACTGTGGCCTTCACCGCCAATTTTCTCCCTTCC CTACTGTCGCCAATTTTCGCCAATTTCTTC CTACTGCCCAATTTTCGCCCAATTTTCCCTTTC CTACTGCCAATTTTCGCCCAATTTTCCTTCC CTACTGCCAATTTTCGCCCAATTTTCCTTTC

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				TAAGACCTCTGAAGACCCTTCAAAACTGGAA			

				GCCAAAGGAACTGGAGGCACTGATTTAATGA ATTTCCTGAAGACTGTAAGAAGTACAACTGAG AAATCCCTTTTGAAGGAAGGTTAA		
Shigella ipaD	4	prey53735	108	TGGATTAC CAAGGCCA GTTACCAA GTTACCAA TGGGCCCC CTGGGCCCA AGGTTCCC STGGCCCA AGGCAGG ACGTCCCG STGCCCG ACGTCCCG ACGTCCCG ACGTCCCG ACGCAAAAC CTCAATCG ACCACCCG ACCACCCG ACCACCCG ACCACCCC ACCACCC ACCACCC ACCACCC ACCACC	608	GEPEGSFVDYQTTMVRTAKAI AVTVQEMYTKSNTSPEELGPL ANQLTSDYGRLASEAKPAAVA AENEEIGSHIKHRVQELGHGC AALVTKAGALQCSPSDAYTKK ELIECARRVSEKVSHVLAALQA GNRGTQACITAASAVSGIIADL DTTIMFATAGTLNREGTETFA DHREGILKTAKVLVEDTKVLVQ NAAGSQEKLAQAAQSSVATIT RLADVVKLGAASLGAEDPETQ VVLINAVKDDAKALGDLISATK AAAGKVGDDPAVWQLKNSAK VMCTNVTSLLKTVKAVEDEAT KGTRALEATTEHIRQELAVFCS PEPPAKTSTPEDFIRMTKGITM ATAKAVAAGNSCRQEDVIATA NLSRRAIADMLRACKEAAYHP EVAPDVRLRALHYGRECANG LTGHSKRVAGSVTELIQAAEA MKGTEWVDPEDPTVIAENELL GAAAAIEAAAKKLEQLKPRAK PKEADESLNFEEQILEAAKSIA AATSALVKAASAAQRELVAQG KVGAIPANALDDGQWSQGLIS AATSALVKAASAAQRELVAQG KVGAIPANALDSSAKQVAASTA QGHASQEKLISSAKQVAASTA QGLVACKVKADQDSEAMKRL QAAGFEQENETVVVKEKMVG
				GTTTCTGTTCCCCAGAGCCACCTGCCAAGA		GIAQIIAAQEEMLRKERELEEA

		COTOTA COCO A CONCETT CATO CON A TONO CONTROL BKK	RKKI AOIROOOYKEI PSFI RD
		CGTTGCTGCCAATTCCTGTCGCCAGGAA	
		GATGTCATTGCCACAGCCAATCTGAGCCGCC	
		GTGCTATTGCAGATATGCTTCGGGCTTGCAA	
		GGAAGCAGCTTACCACCCAGAAGTGGCCCCT	
		GATGTGCGGCTTCGAGCCCTGCACTATGGCC	
		GGGAGTGCCCAATGGCTACCTGGAACTGCT	
		GGACCATGTACTGCTGACCCTGCAGAAGCCA	
		AGCCCAGAACTGAAGCAGCAGTTGACAGGAC	
		ATTCAAAGCGTGTGGCTGGTTCCGTCACTGA	
		GCTCATCCAGGCTGCTGAAGCCATGAAGGGA	1
_		ACAGAATGGGTAGACCCAGAGGACCCCACA	
		GTCATTGCTGAGAATGAGCTCCTGGGAGCTG	
		CAGCCGCCATTGAGGCTGCAGCCAAAAAGCT	
	-	AGAGCAGCTGAAGCCCCGGGGCCAAACCCAA	
		GGAGGCAGATGAGTCCTTGAACTTTGAGGAG	
		CAGATACTAGAAGCTGCCAAGTCCATTGCAG	
		CAGCCACCAGTGCACTGGTAAAGGCTGCGTC	
		GGCTGCCCAGAGAACTAGTGGCCCAAGG	
		GAAGGTGCCATTCCAGCCAATGCACTG	
		GACGATGGGCAGTGGTCCCAGGGCCTCATTT	
	•	CTGCTGCCGGATGGTGGCTGCGGCCACCA	
		ACAATCTGTGTGAGGCAGCCAATGCAGCTGT	
		ACAAGGCCATGCCAGGCAGAAGCTCATC	
		TCATCAGCCAAGCAGGTAGCTGCCTCCACAG	
		CCCAGCTCCTTGTGGCCTGCAAGGTCAAGGC	
-		TGACCAGGACTCGGAGGCAATGAAACGACTT	
	-	CAGGCTGCTGGCAACGCAGTGAAGCGAGCC	
		TCAGATAATCTGGTGAAAGCAGCACAGAAGG	
		CTGCAGCCTTTGAAGAGCAGGAGAATGAGAC	
		AGTGGTGGTGAAAGAGAAGATGGTTGGCGG	
		CATTGCCCAGATCATCGCAGCACAGGAAGAA	
		ATGCTTCGGAAGGAACGAGAGCTGGAAGAG	
		GCGCGGAAGAACTGGCCCAGATCCGGCAG	
		CAGCAGTACAAGTTTC1GCC11CAGAGC11C	

				GAGATGAGCACTAA	
Shigella ipaD	4	prey67574	109	GETTGCAANCGGCGGGT 310 NGNNCGTGNACGANCC SCTGGGTCCTGGGATNC ATNTACNTTNGTCTNTGT SGNTGCACTNCNNNCGT ACAAGACCCCAATTNTGA NGANNTGCCAATTNTGA STNTNAACAC	XQEXELQXAGDAXLPXRXRXT DAXXWVLGXQTTXXXTXVXV RXXXGCTXXVIA*XXXMPRHF XXXIQYHXXX*FXFXXCQX**R EHXXSWELVFLXXVXT
Shigella paC	ა	prey67509	110	GCTACTCACCCACCTCCCAGCTACTCGCC 311 YSPTSI CACCTCTCCCAGCTATTCGCCCACCTCTCCC AGCTACTCCCCACCTTCCCC AGCTACTCCCCACCTTCCCC CCACTTCCCCTAGCTATTCGC CCACTTCCCCTAGCTATTCGC CCACTTCCCCTAGCTATTCGC CCACTTCCCCTAGCTATTCGC CCACCTTCCCCAGCTATTCTC CCACCTTCCCCAGCTATTCTCC CCACCTCCCCAGCTATTCTC CCACCTCCCCCAGCTATTCTC CCACCTCCCCCAGCTATTCT CCCACCTCCCCAGCTATTCT CCCACCTCCCCAGCTATTCC CCACCTCCCCCAGCTATTCC CCACCTCCCCAGCTATTCC CCACCTACTAGTCCCCAGCTATTC CCCACCTACTAGTCCCCAGCTATTC CCCTACTAGTCCCCACTTCCCCAAGCT ACCCACCAGCTCCCCAGCTAC ACCCACCTTCCCAGCTATTCCCCCAAGCT CCCCACCTTCCCAGCTATTCCCCCAAGCT CCCCACCTTCTTATAGTCCCCAAGCT CACCCCAACCTCCCCAGGT CCCCAACCTCCCCAGGT CCCCAACCTCCCCAACCTTCCCCAAGCT CACCCCAACCTCCCCAACCT CCCCAACCTCCCCAACCTTCCCCAAGCT CACCCCAACCTCCCCAACCT CCCCAACCTCCCCAACCTCCCCAACCT CCCCCAACCTCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCAACCTCCCCCAACCT CCCCCAACCTCCCCCC	YSPTSPSYSPTSPSYSPTSPS YSPTSPSYSPTSPSYSPTSPS YSPTSPSYSPTSPSYSPTSPS YSPTSPSYSPTSPSYSPTSPS YSPTSPSYSPTSPSYSPTSPS YSPSSPRYTPQSPTYPTSPS YSPSSPEYTPTSPKYYPTSPS YSPTSPKYSPTSPKYSPTSPK YSPTSPTYSPTYSPTSPK YSPTSPTYSPTSPKYSPTSPT YSPTSPTYSPTSPSPTSPT YSPTSPKGSTYSPTSPTSPT YSPTSPKGSTYSPTSPT YSPTSPKGSTYSPT YSPTSPKGSTYSPT YSPTSPKGSTYSPT YSPTSPKGSTYSPT YSPTSPKGSTYSPT YSPTSPKGSTYSPT YSPTSPKGSTY YSPTSPKGST YSPTSPKGS

				CTCTCCCAAGTACTCACCTACTAGCCCCACTT ACTCGCCCACTTCCCCCAAGTACTCGCCCAC CAGCCCCACTTCCCCCACAC GGCTCACTCTCCCCACAC GGCTCACCTCCCCCACA ACTCGCCCACCTCCCCCACAC AAGCCCACCACCTCCCCGGATGACACCCCCCCCACACCCACC		
Shigella ipaC	മ	prey67514	111	4		MHKEEHEVAVLGAPPSTILPR STVINIHSETSVPDHVVWSLFN TLFLNWCCLGFIAFAYSVKSR DRKMVGDVTGAQAYASTAKC LNIWALILGILMTIGFILSLVFGS VTVYHIMLQIIQEKRGY*
Shigella ipaC	ഗ	prey2926	112	ATGGAGAAACTTGTATAGATGCACTTCCTCT TACTATGAATTCTTCAGAAAAGCAAGAGACTG TATGTATTTTTGGAACTGGTGATTTTGGAAGA TCACTGGGATTGAAAATGCTCCAGTGTGGTT ATTCTGTTGTTTTTTGGAAGTCGAAACCCCCAG AAGACCACCCTACTGCCCAGTGGTGCAGAG TCTTGAGCTATTCAGAAGCAGCCAAGAAG TCTTGAGCTATTCAGAAGCAGCCAAGAAG TCTTGAGATTTTCTCACAGAATTAACTGAGG CATTATGATTTTCTCACAGAATTCACAGAA ACAACCTCAAAATTTGGTAGCAATCCAGCA ACAACCTCAAAATCATTGGTAGCAATCT AATGCAGAGTACCTTGCTCATTTGGTGCCAG GAGCCCACGTGGTAAAAAGCATTTAACAGA CTCAGCCTGGGTAAAAAGCATTTAACAGA CTCAGCCTGGGTAAAAAGCATTTAACACCAT CTCAGCCTGGGCTCTCCAGTTTGTGTGTGTGGAA	8	MEKTCIDALPLTMNSSEKGET VCIFGTGDFGRSLGLKMLQCG YSVVFGSRNPQKTTLLPSGAE VLSYSEAAKKSDIIIIAIHREHYD FLTELTEVLNGKILVDISNNLKI NQYPESNAEYLAHLVPGAHVV KAFNTISAWALQSGALDASRQ VFVCGNDSKAKQRVMDIVRNL GLTPMDQGSLMAAKEIEKYPL QLFPMWRFPFYLSAVLCVFLF FYCVIRDVIYPYVYEKKDNTFR MAISIPNRIFPITAPYTACFGLP PWCYCCHSTTVPRHKIPSIPR LA*

				ATGACAGCAAAGCCAAAGAGTGATGGA TATTGTTCGTAATCTTGGACTTACTCCAATGG ATCAAGGATCACTCATGGCAGCCAAAGAAAT TGAAAAGTACCCCTGCAGCTATTTCCAATGT GGAGGTTCCCCTTCTATTGTCTGTTATAAG AGACGTAATCTACCTTATTGTTTATGAAAAGA AAGATAATACATTTCGTATTGTTTTCCATT CCAAATCGTATCTTCCAATAACAGCACCTTA CACTGCTTGGTTTACCATTACAATAACAGCACCTTA		
Shigella ipaC	ഗ	prey4458	113	0	314	QDVQASQAEADQQQTRLKEL ESQVSGLEKEAIELREAVEQQ KVKNNDLREKNWKAMEALAT AEQACKEKLHSLTQAKEESEK QLCLIEAQTMEALLALPELSV L
Shigella ipaC	വ	prey4458	411	GAGCACACTGCAGGC CCCAGCATCCTGGC GCTCAGAGACCTGCA GGAGGAGCAGCTGTG GGAGGAGCAGGTGTG CGCCGCAGGAGGAGG SGGTCACAGTGAAGCA	315	AEETQSTLQAECDQYRSILAE TEGMLRDLQKSVEEEEQVWR AKVGAAEEELQKSRVTVKHLE EIV
Shigella ipaC	2	prey67522	115	GANGAATNCNNTATGCCAAAAGGACAAGGAG GTATTGGTNGCTTANGCTGGCTATGAATACN TCNTTCTGTTTGTGATANTCTATTCTTACACC NTCNGGCATGGTAGGCAANNGCCACAGTANA TGCCACATCTATGAGGCAANNGCCACAGTANA	316	XEXXMPKGQGGIGXLXWL*IX XSVCDXLFLTPSGMVGXXHSX CHIYEAXAAYSPCLXTSXLXXX ARXVPXDXVXXTAWCXTXRT AXTXTSWRTYHEXMLTLVGRL

				CGCCGTGTCTANCTACATCCTNGTTANNGGN TGNGGCCCGNNCGGTTCCTNCCGATTNTGTT CNGGNCACAGCCTGGTGTNTGACANCTCGG ACCGCGNTNACTATNACCTCCTGGAGGACCT ACCACGAANGCATGCTNACCTCGGTGGGGGA GGCTGGAAGG		ш
Shigella ipaC	رم د	prey527	116	10 10 10 10 10 10 10 10 10 10 10 10 10 1	317	MTADLPNELIELLEKIVLDNSVF SEHRNLQNLLILTAIKADRTRV MEYINRLDNYDAPDIANIAISNE LFEEAFAIFRKFDVNTSAVQVL IEHIGNLDRAYEFAERCNEPAV WSQLAKAQLQKGMVKEAIDS YIKADDPSSYMEVVQAANTSG NWEELVKYLQMARKKARESY VETELIFALAKTNR
Shigella ipaC	വ	prey53735	117	TGAG AGCC SATG SGCTG AGCC CAGA SAGTT GTAAC GGAG	318	AVGEISHLIEPLANAARAEASQ LGHKVSQMAQYFEPLTLAAVG AASKTLSHPQQMALLDQTKTL AESALQLLYTAKEAGGNPKQA AHTQEALEEAVQMMTEAVED LTTTLNEAASAAGVVGGMVDS ITQAINQLDEGPMGEPEGSFV DYQTTMVRTAKAIAVTVQEMV TKSNTSPEELGPLANQLTSDY GRLASEAKPAAVAAENEEIGS HIKHRVQELGHGCAALVTKAG

		ALGCSPSDATTRALEICON IN THE PROPERTY OF THE PRO
	AGGCAGCCAG GC	VSEKVSHVLAALQAGNRGTQ
	CCAGCTAGATGAGGACCAATGGGTGAACCA	ACITAASAVSGIIADLDTTIMFA
	GAAGGTTCCTTCGTGGATTACCAAACAACTAT	TAGTLNREGIEIFADHREGIL
	GGTGCGGACAGCCATTGCAGTGAC	KTAKVLVED I KVLVQINAAGSQ
	CGTTCAGGAGATGGTTACCAAGTCAAACACC	EKLAGAAGSSVATTI KLADVVK
	AGCCCAGAGGAGCTGGGCCCTCTTGCTAAC	LGAASLGAEDPE I QV VEII AV
	CAGCTGACCAGTGACTATGGCCGTCTGGCCT	KDVAKALGDLISA I NAMAGNV
	CGGAGGCCAAGCCTGCAGCGGTGGCTGCTG	GDDPAVWQLKNSAKVMVINV
	AAAATGAAGATAGGTTCCCATATCAAACAC	TSLLKTVKAVEDEATKGTRAL
_	CGGGTACAGGAGCTGGGCCATGGCTGTGCC	EATTEHIRGELAVECSPEPPAK
	GCTCTGGTCACCAAGGCAGGCGCCCTGCAG	TSTPEDFIRMTKGITMATAKAV
	TGCAGCCCCAGTGATGCCTACACCAAGAAGG	AAGNSCROEDVIATANLSRRA
-	AGCTCATAGAGTGTGCCCGGAGAGTCTCTGA	IADMLRACKEAAYHPEVAPUV
	GAAAGTCTCCCACGTCCTGGCTGCGCTCCA	RLRALHYGRECANGYLELLU
	GGCTGGGAATCGTGGCACCCAGGCCTGCAT	
	CACAGCAGCCAGCGCTGTGTCTGGTATCATT	
	GCTGACCTCGACACCACCATCATGTTCGCCA	
	CTGCTGGCACGCTCAATCGTGAGGGTACTGA	
_	AACTTTCGCTGACCACCGGGAGGGCATCCTG	
. —	AAGACTGCGAAGGTGCTGGTGGAGGACACC	
	AAGGTCCTGGTGCAAAACGCAGCTGGGAGC	
	CAGGAGAAGTTGGCGCAGGCTGCCCAGTCC	
	TCCGTGGCGACCATCACCCGCCTCGCTGATG	
	TGGTCAAGCTGGGTGCAGCCAGCCTGGGAG	
	CTGAGGACCCTGAGACCCAGGTGGTACTAAT	
	CAACGCAGTGAAAGATGTAGCCAAAGCCCTG	
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	CTCGGGCCCTGGAGCCACCACAGAACACA	
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				AGCCAATCTGAGCCGCCGTGCTATTGCAGAT	
				ATECTTCGGGCTTGCAAGGAAGCAGCTTACC	
				ACCCAGAAGTGGCCCCTGATGTGCGGCTTC	
				GAGCCCTGCACTATGGCCGGGAGTGTGCCA	
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Shinella	5	prey53735	118	-	SDVLDRASSLIEERNISAGI II
inac	•			CATTGAGGAGGCGAAAAGGCAGCTGGCCA	GUPESQUALLACANANA
O Pad				TCCAGGGGACCCTGAGAGCCAGCAGCGGCT	NRCVSCLPGGRDVDNALKAV
				TGCCCAGGTGGCTAAAGCAGTGACCCAGGC	GDASKRLLSDSLPPS1G1FUE
				TCTGAACCGCTGTCAGCTGCCTACCTGGC	AGSRLNEAAAGLNGAATELVO
				CAGGGGATGTGGATAATGCCCTGAGGGCA	ASRGTPODLARASGRFGQDF
				GTTGGAGATGCCAGCAAGCGACTCCTGAGTG	STFLEAGVEMAGQAPSQEDR
				ACTOROTTOCTOCTAGGACTTGA	AQVVSNLKGISMSSSKLLLAAK
				AGAAGCTCAGAGCCGGTTGAATGAAGCTGCT	ALSTDPAAPNLKSQLAAAARA
				POT TREE CT TO A TO A GO CA CAGA A CT G	VTDSINGLITMCTQQAPGQKE
				PATECAGGCTCTCGGGGAACCCCTCAGGAC	CDNALRELETVRELLENPVQPI
				CTGGCTCGAGCCTCAGGCCGATTTGGACAG	NDMSYFGCLDSVMENSKVLG
				GACTTCAGCACCTTCCTGGAAGCTGGTGTGG	EAMTGISONAKNGNLPEFGDA
				AGATGGCAGGCCAGGCTCCGAGCCAGGAGG	ISTASKALCGFTEAAAQAAYLV
				ACCGAGCCCAAGTTGTGTCCAACTTGAAGGG	GVSDPNSQAGQQGLVEPTQF
				CATCTCCATGTCTTCAAGCAAACTTCTTCTGG	ARANQAIQMACQSLGEPGCT
				CTGCCAAGGCCCTGTCCACGGACCCTGCTG	QAQVLSAATIVAKHTSALCNS
				CCCTAACCTCAAGAGTCAGCTGCTGCAGC	CRLASARTTNPTAKKUFVUSA
				TGCCAGGGCAGTAACTGACAGCATCAATCAG	KEVANSTANLVKTIKALDGAFI
				CTCATCACTATGTGCACCCAGCAGGCACCCG	EENRAQCRAA APLLEAVUNL
				GCCAGAAGGAGTGTGATAACGCCCTGCGGG	SAFASNPETSSIPACISPEGRA
				AATTGGAGGCGGTCCGGGAACTCCTGGAGAA	AMEPIVISAKTMLESAGGLIQT
		_		CCCAGTCCAGCCCATCAATGACATGTCCTAC	ARALAVNPRD
				TTTGGTTGCCTGGACAGTGTAATGGAGAACT	
				CAAAGGTGCTGGGCGAGGCCATGACTGGCA	
				TCTCCCAAAATGCCAAGAACGGAAACCTGCC	
				AGAGTTTGGAGATGCCATTTCCACAGCCTCA	
				AAGGCACTTTGTGGCTTCACCGAGGCAGCTG	

ۍ	prey67546	CCCCAATAGCCAAGCTGGACAGCAAGGGCTA GTGGAGCCCACAGGTTTGCCGGTGCAAACC AGGCAATTCAGATTGCCCGTGCAAACC AGGCCATTCAGATTGCCCAGGTTTGGG AGGCCTGTGTACCCAGGCCCAGGTGCT CTGCAGCCTGTTGTGCCCAGGTGCT CTGCACTGTTGTACAGCTGTCGCCAAGCG CCAGTTTGTACAGTCAATCCTACTGCCAAGCG CCAGTTTGTACAGTCTACTGCCAAGGC AACAGCACAGC	TGADLLEEHLGEIWNLRQRLE
un un			ESICINDCLREQLEHR LESLIQRVSQLEAQLPKNGLEE KLAEELRSASWPGKYDSLIQD QARELSYLRQKIREGRGICYLI TRHAKDTVKSFEDLLRSNDID YYLGQSFREQLAQGSQLTERL TSKLSTKDHKSEKDQAGLEPL ALRLSRELQEKEKVIEVLQAKL DARSLTPSSSHALSDSHRSPS STSFLSDELEACSDMDIVSEYT HYEEKKASPSHSDSIHHSSHS SNPISL PTPQNTPKEANQAHS

				TACTTGAGCCACTGGCCCTCAGGCAG		GEHFHSIPKLASLPQAPLPSAP
				GGAGCTGCAGGAGGAGGAGAAGTGATTGA		SSFLPFSPTGPLLLGCCETPV
				AGTCCTGCAGGCCAAGCTGGATGCTCGGTC		VSLAEAQQELQMLQKQLGES
				CCTCACACCCTCCAGCAGCCATGCCTTGTCT		ASTVPPASTATLLSNDLEADS
				GACTCCCACCGCTCTCCCAGCAGCACCTCTT		SYYLNSAQPHSPPRGTIELGRI
				TCCTGTCTGATGAACTGGAAGCCTGCTCTGA		LEPGYLGSSGKWDVMRPQKG
		-		CATGGACATAGTCAGCGAGTACACACACTAT		SVSGDLSSGSSVYQLNSKPTG
				GAAGAGAAGAAGCTTCTCCCAGTCACTCAG		ADLLEEHLGEIRNLRQRLEESI
				ATTCCATCCATCATTCGAGTCATTCTGCTGTG		CINDRLREQLEHR
				TTGTCTTCTAAACCATCATCAACCAGTGCATC		
			_	TCAGGGGCTAAGGCCGAATCCAACAGCAA		
				CCCCATCAGCTTGCCAACTCCCCAGAATACC		
				CCCAAGGAGGCCAACCAGGCCCATTCAGGC		
			_	TITCATTITCACTCCATACCCAAGCTGGCTAG		
			_	ccrrccrcaggcaccattgcccrcagcrcca		
			_	TCCAGCTTCCTGCCTTTCAGCCCCACTGGCC		
			_	CTCTCCTCCTTGGCTGCTGTGAGACACCAGT		
			_	GETCTCCTTGGCTGAGGCTCAGCAGGAGCTA		
				CAGATGCTGCAGAAGCAGTTGGGAGAAGTG		
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				ATTGCTGAGCAACGACTTGGAAGCCGACTCT		
			-	TCCTACTACCTCAACTCTGCCCAGCCTCACT		
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				AATCCTAGAGCCTGGGTACCTGGGCAGCAGT		
				GGCAAGTGGGATGTGATGAGGCCTCAGAAA		
		-		GGGAGTGTATCTGGGGACCTATCCTCAGGCT		
				CCTCTGTGTACCAGCTTAACTCCAAACCCAC		
				AGGGGCTGACCTGCTGGAAGAGCATCTTGGT		
				GAAATCCGGAACCTGCGCCAGCGCCTGGAG		
				GAGTCCATCTGCATCAATGACCGCCTACGGG		·
Shigella	5	prey67550	121		322	MLTELLFELHVAATPDKLNKA
ipaC				GGCGGCCACACCTGACAAACTCAATAAGGCC		MKRAHDWVEEDQTVVSVDVA
				ATGAAGAGGGCTCATGACTGGGTGGAAGAG		KVSEEETKKEEKEEKSQDPQE
				GATCAAACCGTGGTGTCAGTAGATGTGGCAA		DKKEEKKTKTIEEVYMSSIESL

		-	CATOCOLATOROGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGO	RO	ROWLOEAMSAAFRGGREEVE
			AGACCCTCCTCCAGAACCGATGAGTGAGGAG	Wo	QMKSCLRVLSQPMPPTAGEA
-	_		AGGCGTCAGTGGCTGCAGGAGGCCATGTCG	EO	EQAADQQEREGALELLADLCE
			GCTGCCTTCCGAGGCCAGCGGGGGGGGG	Z	NMDNAADFCQLSGMHLLVGR
			GAGCAGATGAAGAGCTGCCTCCGAGTGCTGT	Y.E.	YLEAGAAGLRWRAAQLIGTCS
			CACAGCCCATGCCCCCACTGCTGGGGAGG	NO_	ONVAAIOEOVLGLGALRKLLR
			CCGAGCAGGCGGCCGACCAGCAGAGAGCGAG	<u> </u>	LLDRDACDTVRVKALFAISCLV
			AGGGGCCCTGGAGCTGCTGGCCGACCTGT	RE	REQEAGLLQFLRLDGFSVLMR
			GTGAGAACATGGACAATGCCGCAGACTTCTG	AM	AMOQOVOKLKVKSAFLLONLL
			CCAGCTGTCTGGCATGCACCTGCTGGTGGG	<u>Ne</u>	VGHPEHKGT
			CCGGTACCTGGAGGCGGGGGCTGCGGGGACT		
			GCGGTGGCGGCGCACAGCTCATCGGCAC		
			GTGCAGTCAGAACGTGGCAGCCATCCAGGA		
			GCAGGTGCTGGGCCTGGGTGCCCTGCGTAA		
			GCTGCTGCGGCTGCTGGACCGCGACGCCTG	-	
			CGACACGGTGCGCGTCAAGGCCCTCTTCGC		
			CATCTCCTGTCTGGTCCGAGAGCAGGAGGCT		
			GGGCTGCTGCAGTTCCTCCGCCTGGACGGC		
			TTCTCTGTGTTGATGAGGGCCATGCAGCAGC		
			AGGTGCAGAAGCTCAAGGTCAAATCAGCATT		
			CCTGCTGCAGAACCTGCTGGTGGGCCACCC		
Shinella 5	prev67473		124 ATGGCAGAGAAGGTGCTGGTAACAGGTGGG 325		MAEKVLVTGGAGYIGSHIVLE
ipaC				38	LLEAGYLPVVIDNFHNAFKGG
			GAGCTGCTGGAGGCTGGCTACTTGCCTGTG	23 i	GSLPESLKKVÜELTGKSVETE
			GTCATCGATAACTTCCATAATGCCTTCCGTGG	. E	EMDILDGGALGRLFRKTSFIMA
			AGGGGCTCCCTGCCTGAGAGCCTGCGGCG		VIHFAGLKAVGESVOKPLDYY
			GGTCCAGGAGCTGACAGGCCGCTCTGTGGA	Σ !	KVNLI GIIQLLEIMKAHGVNNL
			GTTTGAGGAGATGGACATTTTGGACCAGGGA	\	VESSSATVYGNPQYLPLDEA
			GCCCTACAGCGTCTCTTCAAAAAGTACAGCT		
			TTATGGCGGTCATCCACTTTGCGGGGCTCAA	-	
			GECCETGEGCGAGTCGGTGCAGAAGCCTCT		
			GGATTATTACAGAGTTAACCTGACCGGGACC		
			ATCCAGCTTCTGGAGATCATGAAGGCCCACG		
			GGGTGAAGAACCTGGTGTTCAGCAGCTCAGC		

	KVVQRLVERGRSLDDARKRA KQFHEAWSKLMEWLEESEKS LDSELEIANDPDKIKTQLAQHK EFQKSLGAKHSVYDTTNRTGR SLKEKTSLADDNLKLDDMLSE LRDKWDTICGKSVERQNKLEE ALLFSGQFTDALQALIDWLYR VEPQLAEDQPVHGDIDLVMNL IDNHKAFQKELGKRTSSVQAL KRSARELIEGSRDDSSWVKVQ MQELSTRWETVCALSISKQTR LEAALRQAEEFHSVVHALLEW LAEAEQTLRFHGVLPDDEDAL RTLIDQHKE	LTHTEELLDAGKPISGDPKVIE VELAKHHVLKNDVLAHQATVE TVNKAGNELLESSAGDDASSL RSRLEAMNQCWESVLQKTEE REQQLQSTLQQAGFHSEIED
	356	327
CACTGTGTACGGGAACCCCCAGTACCTGCCC	AAAAGTGGTTCAACGGTTGGTAGAGAGAGGGA AGATCTTTGGATGATGCAAGGAAGAGACCA AGCAGTTCCATGAAGCTTGGAAAAGTCTTTG GGAGTGGCTAGAAGGTCAGAAAAGTCTTTG GGAGTTCCAGAAAACCTCCAAACATGATCCAG ACAAAAAAAAACACACCAACAACATAG GAGTTTCAGAAATCACTCGGAGCCAACATT CTGTCACGACACCACCACAGCATT CTGTCTACGACACTGGATGGAT GACAACCTGAAACTGGATGGAT GACAACCTGAAACTGGATGCGAT TCTCTGAAGGAGAAACCTCCCTGGCTGAT GACAACCTGAAACGGATCCCTGGTGAT GACACCTGAAACTGGATGGAT GACACCTGAAACGGATCCCTGGTGAT TGCCTACGAGACAATTGGATGGAT GACACCTGTTATTTTCTGGACAATTGGAG AAATCTGTGGAAAGCAAATGGAA TGCCTACAGGCTCTCATTGATTGGTGATGAA GAGCCTTCATGGAAATGGCAAAAAG AGGCAATGGACACTCCTGGGTCAA AGGCAATGCGAAATTAACAAAGC AGGCAATGCAGAATTAACAAAGC AGGCAAGCCCTCCGGGGAACTCATAGA AGCCGTTAGAACCCCTCCTGGGTCAA AGCCGTTAGAACCCCTCCTGGGTCAA AGCCGTTAGAACCCCTCCTGGGTCAA AGCCGTTAGAACCCCTCCCTGGGCCCC TTGGAGTGCCTGGGGCGAACCC TTGGAGTGCCTCGGTGGTCAAACC CTGCGTTTCCATGGTGATCAAACC CTGCGTTTCCATGGTGTCCCCCCCCCTCC CTGCGTTTCCATGGTGTCCCCCCCCCC	GCTGACTCATACCGAAGAGTTGTTAGATGCT CAGAGACCAATAAGTGGAGACCCAAAAGTCA TTGAAGTTGAGCTCGCAAAGCACCATGTCCT AAAAAATGATGTTTTGGCTCATCAAGCCACAG TGGAAACAGTCAACAAAGCTGGCAATGAGCT
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	TCTTGAATCCAGTTTTGGAAGCCATGAACC	PETAREQLDTHMELYSQLKAK
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_	CONTRACTOR CON	GSGSKTEQSVALLEQKWHVV
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	GAAGATTCCTCTTGGAACTTACTAGAATGGA	QNSLQEFINWLTLAEQSLNIAS
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TG SGC SAG SAG STG CT SCT SCT SGC SAG SGC SAG SGC SAG SGC SAG SGC SGC SGC SGC SGC SGC SGC SGC SGC SG	EKEELPRAVGTQTLSGAGLLK MFNKATDAVSKMTIKMNESDI CA CA SA
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	127
	prey3514
	ن
	Shigella ipaC

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				ACTCACAGCAGCTGGCAAAGTACTGGGA		
				AGCCTTCCTTCCTGAGGCAAAGGCCATCTCC		
Shigella	5	prey5814	128	1	329	DAPPOI ENEEDAEDITEI AKI
ipaC				CCTGCATTTCCACATACTGACTTGGCCAAGTT	3	DOMINRPRWAVAVI PKGEI EV
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Shigella	5	prey5814	129	CCATGCCAAACTTGGAGAAAGCAGCCTTAGT 330	HAKLGESSLSPSLDSLFFGPS
ipaC				CCATCTTGACTCACTTTTCTTTGGTCCTTC	ASQVLYLTEVVYALLMPAGAP
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•			<u>∢</u>	AATCACTATCAAAAAAGAGCATACCAGTGTAT		
-				AAAATGTATGGTAGCTCTATTTAGTAACTGTC		
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			<u> </u>	TACAGGCCCAGCAGCACATCACATGAACAAC		
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		-	⋖	ATTATGAAGGCAGTGAAGAAGTATCCCCACC		
			<u> </u>			
	5	prey67479	130 C	CGATGAGCTCATGAGACATCAGCCCACCCTT 331	DELMRHQPTLKTDATTAIIKL	AIIKL
ipaC			⋖	AAAACAGATGCAACGACTGCCATCATCAAGT	EEICNLGRDPKYICQKPSIQKA	SIOKA
			<u> </u>	TACTTGAAGAAATCTGTAATCTTGGAAGGGAC	DGTATAPPPRSNHAAEEASSE	EASSE
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•			_	TCTAGTGAGGATGAGGAGGAAGAGTAC	EFVNQKGLLPLVTILGLPNLPID	PNLPID
			⋖	AGGCCATGCAGAGCTTTAATTCTACCCAGCA	FPTSAACQAVAGVCKSILTLSH	ILTLSH
			<u> </u>	AAATGAAACTGAGCCTAATCAGCAGGTTGTT	EPKVLQEGLLQLDSILSSLEPL	SLEPL
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				TTCAAGAGGGTCTCCTTCAGTTGGACTCCAT	
				一	
Shidella	5	prey700	131	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGA 332	MGIGLSAGGVNMNRLPGWDR
ipaC	k	•		ACATGAATAGACTACCAGGTTGGGATAAGCA	HSYGYHGDDGHSFCSSG1GQ
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Shinella	5	prev67481	132	t	KODOKAPDKEAILRATANLPS
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Shigella ipaC	ഗ	prey67488	133		334	LFMKSERHAAEAQLATAEQQL RGLRTEAERARQAQSRAQEA LDKAKEKDKKITELSKEVFNLK EALKEQPAALATPEVEALRDQ VKDLQQQLQEAARDHSSVVA LYRSHLLYAIQ
Shigella ipaC	മ	prey51967	134	TGACCAACTTGTGTTGATATTTGCTGGAAAAA TTTTGAAAGATCAAGATACCTTGAGTCAGCAT GGAATTCATGATGGACTTACTGTTCACCTTGT CATTAAAACACAAAACAGGCCTCAGGATCATT CAGCTCAGCAAACAGCTGGAGCAA TGTTACTACATCATCACTCCTAATAGTAACT CTACATCTGGTTCTGCTACTAGCAACCCTTTT GGTTTAGGTGGCCTTGGGGGACTTGCAGGT CTGAACTACAGCAGTTCACAGCAACCTTT CTGAACTACAGCAGTTGAATACTACCAACT CTGAACTACAGAGTCAGATGCAGGT CTGAACTACAGAGTCAGATGCAGGT CAGGAAATTGTTGTTCAGAGCATGCTCT CAATCCTGACCTGA	335	DQLVLIFAGKILKDQDTLSQHG IHDGLTVHLVIKTQNRPQDHSA QQTNTAGSNVTTSSTPNSNST SGSATSNPFGLGGLGGLAGLS SLGLNTTNFSELQSQMQRQLL SNPEMMVQIMENPFVQSMLS NPDLMRQLIMANPQMQQLIQR NPEISHMLNNPDIMRQTLELA RNPAMMQEMMRNQDRALSN LESIPGGYNALRRMYTDIQEP MLSAAQEQFGGNPFASLVSN TSSGEGSQPSRTENRDPLPN PWAPQTSQSSSASSG

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Shigella	2	prey6/491			ATNITCIATVPPOPOYSYHDI
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				TGAGATGGACAAGAGATTAGCAACTGAATTT	
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				GCAGATACTGTGATCCTGTTGTTTTAACATAT	
				CAAGCTGAACGGATGCCAGAGCAAATCAGGC	
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	-			GGCTGTTTACGAAGAGTTTGCACGCAATGTT	
				CCTGGCTTCTTACCTACAATGACTTAAGTCA	

				GCCCACGGGATTTTTAGCCCAGCCCATGAAG CAAGCTTGGGCAACAGATGATGTAGCTCAGA		
				TTTATGATAAGTGTATTACAGAACTGGAGCAA		
				CATCTACATGCCATCCCACCAACTTTGGCCAT		
				GAACCCTCAAGCTCAGGCTCTTCGAAGTCTC		
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				GACAGCGATGACTATCACCTCCTAAAGGACC		LLYCFRKDMDKVETFLRMVOC
				TAGAGGAAGGCATCCAAACGCTGATGGGGA		RSVEGSCGF*
				GGCTGGAAGACGGCAGCCGCCGGACTGGGC		
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				CACAAACTCGCACAACCATGACGCACTGCTC		
				AAGAACTACGGGCTGCTCTACTGCTTCAGGA		
				AGGACATGGACAAGGTCGAGACATTCCTGCG		
				CATGGTGCAGTGCCGCTCTGTGGAGGGCAG		
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Shigella	2	prey67495	137	GCAGCAGTCTCTGTGCTGAAACCCTTCTCCA	338	AAVSVLKPFSKGAPSTSSPAK
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				GACTTAACCCACGCTATTTCCATTTTAGAAAG		FHKTRSHVTHRTPKVKKSPKV
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				TCTAAACCAATCGTACATGCCAGAAAAAATA		
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				AGGTCAGAAAGAAAGTTATCTGAGTA		
Shigella	2	prey67506	138	GAGAGCCATCCCCAATCAGGGGGGGAGATCCT	339	RAIPNOGEILVIRRGWLTINNIS
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	GATGACAACTGCCTCAGCCAGATGGAACAA	
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				CCCAGAGAGGCCTGGCCCCCAGCCCAACAGC		DEVDENETRY OTALI CLERKIN
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				AAGCCCTTGCACCTAGAAGCCTCTCTGGATA		DOINT EDITANGALAGIMADUAE FEEDGTGSDOI NIND*
				AGGAGATCTATTACCATGGAGAACCCATCAG		
				CGTCAACGTCCACGTCACCAACACCACCAAC		
				AAGACGGTGAAGAAGATCAAGATCTCAGTGC		
-				GCCAGTATGCAGACATCTGCCTTTTCAACAC		
				AGCTCAGTACAAGTGCCCTGTTGCCATGGAA		
				GAGGCTGATGACACTGTGGCACCCAGCTCG		
				ACGTTCTGCAAGGTCTACACACTGACCCCCT		
				TCCTAGCCAATAACCGAGAGAAGCGGGGCCT		
				CGCCTTGGACGGGAAGCTCAAGCACGAAGA		
				CACGAACTTGGCCTCTAGCACCCTGTTGAGG		
				GAAGGTGCCAACCGTGAGATCCTGGGGATC		
				ATTGTTTCCTACAAAGTGAAAGTGAAGCTGGT		

				GGTGTCTCGGGGCGGCCTGTTGGGAGATCT		
				CTTCACCCTAATGCACCCCAAGGCCCAAAGAG		
				GAACCCCGCATCGGGAAGTTCCAGAGAAC		
				GAGACGCCAGTAGATACCAATCTCATAGAAC		
				TTGACACAAATGATGACGACATTGTATTTGAG		
				GACTTTGCTCGCCAGAGACTGAAAGGCATGA		
				AGGATGACAAGGAGGAAGAGGAGGATGGTA		
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Snigella	٥	prey67731	148	ATGTCAATAGCAGGAGTTGCTGCTCAGGAGA	349	MSIAGVAAOFIRVPI KTGEI HN
рану.8				TCAGAGTCCCATTAAAAACTGGATTTCTACAT		GRAMGNMRKTYWSSRSFFK
				AATGGCCGAGCCATGGGGAATATGAGGAAG		NNFLNIDPITMAYSI NSSADER
				ACCTACTGGAGCAGTCGCAGTGAGTTTAAAA		LIPLGHASKSAPMNGHCFAEN
				ACAACTTTTAAATATTGACCCGATAACCATG		GPSOKSSLPPI LIPPSFNI GPH
				GCCTACAGTCTGAACTCTTCTGCTCAGGAGC		EEDOVVCGFKKI TVNGVCAST
				GCCTAATACCACTTGGGCATGCTTCCAAATCT		PPLTPIKNSPSL FPCAPI CFRG
•				GCTCCGATGAATGGCCACTGCTTTGCAGAAA		SRPLPPLPISEAL SLUDTDCEV
				ATGGTCCATCTCAAAAGTCCAGCTTGCCCCC		EFLTSSDTDFLLEDSTLSDFKY
				TCTTCTTATTCCCCCAAGTGAAAACTTGGGAC		DVPGRRSFRGCGQINYAYFDT
				CACATGAAGAGGATCAAGTTGTATGTGGTTTT		PAVSAADLSYVSDONGGVPD
				AAGAAACTCACAGTGAATGGGGTTTGTGCTT		PNPPPPQTHRRLRRSHSGPA
				CCACCCTCCACTGACACCCATAAAAACTC		GSFNKPAIRISNCCIHRASPNS
				CCTTCCCTTTTCCCCTGTGCCCCTTTGTG		DEDKPEVPPRVPIPPRPVKPD
	· · · ·			AACGGGGTTCTAGGCCTCTTCCACCGTTGCC		YRRWSAEVTSSTYSDEDRPP
				AATCTCTGAAGCCCTCTCTCTGGATGACACA		KVPPREPLSPSNSRTPSPKSL
				GACTGTGAGGTGGAATTCCTAACTAGCTCAG		PSYLNGVMPPTQSFAPDPKYV
				ATACAGACTTCCTTTTAGAAGACTCTACACTT		SSKALQRQNSEGSASKVPCIL
				ICIGATITCAAATATGATGTTCCTGGCAGGCG		PIIENGKKVSSTHYYLLPERPP
				AAGCTTCCGTGGGTGTGGACAAATCAACTAT		YLDKYEKFFREAEETNGGAOI
				GCATATTTGATACCCCAGCTGTTTCTGCAGC		QPLPADCGISSATEKPDSKTK
				AGATCTCAGCTATGTGTCTGACCAAAATGGA		MDLGGHVKRKHLSYVVSP*
				GGTGTCCCAGATCCACCTCCACCTC		
				AGACCCACCGAAGATTAAGAAGGTCTCATTC		
				GGGACCAGCTGGCTCCTTTAACAAGCCAGCC		
				ATAAGGATATCCAACTGTTGTATACACAGAGC		

	SRTSLLLAFALLCLPWLQEAG AVQTVPLSRLFDHAMLQAHRA HQLAIDTYQEFEETYIPKDQKY SFLHDSQTSFCFSDSIPTPSN MEETQQKSNLELLRISLLIES WLEPVRFLRSMFANNLVYDTS DSDDYHLLKDLEEGIQTLMGV RVAPGVANPGTPLA*
	350
TTCTCCTAACTCCGATGAAGACAAACCTGAG GTTCCCCCAGAGTTCCCATACCTCCTAGAC CAGTAAAGCCAGATTATAGAAGATGGTCAGC AGAAGTTACTTCGAGCACCTATAGTGATGAA GACAGGCCTCCCAAGAGACC TTTGTCACCGAGTAACTCGCCCACAGAGAC CTTTGTCACCGAGTAACTCGCCACACGAG TCCCAAAAGCTTCCGTCTTTGCCCCTG ATCCCAAGTATGTCAGCACACAGAGG GTCATGCCCCGACACAGAGCATTGCCCCTGCAAGACAGAACAGAACAGAACAGCACACACA	GCTCCCGGACGTCCCTGCTCCTGGCTTTTGC CCTGCTCTGCCTGCTCCAAGAGGGT GGTGCCGTCCCTGGCTTCAAGAGGGCT GGTGCCGTCCAAACCGTTCCGTT
TTCTO GTTCC CAGTA AGAGG CTTTG TCCCA AAGAC GAAGA TACCT TGAAA TGAAA TGAAA TGAAA	GCTCC CCTGC GGTGC TTTTTG CCGCGC GAGTTT CCTCCT CTCCT CTCCT TTCCTC TTCCTC TTCCTC TTCCTC TTCCTC TTCCTC TTCCTC
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	Shigella ipaH9.8

43.40.	NSQRDTLVHLFAGGCGGTVG AAA ALTCPLEVVKTRLQSSSVTLYI SEVQLNTMAGASVNRVVSPG NTTA RHCLKVILEKEGPRSLFRGLG PNLVGVAPSRAIYFAAYSNCK EKLNDVFDPDSTQVHMISAAM AGFTAITATNPIWLIKTRLQLDA RNRGERRMGAFECVRKVYQT DGLKGFYRGMSASYAGISETV IHFVIYESIKQKLLEYKTASTME NGEESVKEASDFVGMMLAAA TSKTCATTIAYPHVVRTRLREE CTG CAA
	A I GAGCCAGAGGGACACGCTGGTGCATCTGT TIGCCGGAGGATGTGGTGGTACAGTGGGAG CTATTCTGACATGTCCACTGGAAGTTGTAAAA ACACGACTGCAGTCATCTTCTGTGACGCTTTA TATTCTGAAGTTCAGCTGAACACCATGGCTG GAGCCAGTGTCAAAGGTGATCTTGGAAA ACCTCTTCATTGCTAAAGGTGATCTTGGAAA AGAAGGGCCTCGTTCCTTGTTTGGAGGACT AGGCCCCAATTTAGTGGGGGTAGCCCTTCC AGGCAATATACTTGCTGCTTATTCAAACTG CAAGGAAAAGTTGATGATTTGATCTGA ATCTACCCAAGTACATGATTTCAGCTGCA ATGGCCAGGTTTTACTGCAATCCAGCCAACCCA
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			ACCCCATTIGGCTTATAAAGACTCGGTTACAG CTTGATGCAAGGAACCGCGGGGAAAGGCGA		SLYRGLTTHLVRQIPNTAIMMA TYELVVYLLNG*
			TCAGACAGATGGACTAAAAGGATTTTATAGG		
			GGCATGTCTGCTTCATATGCTGGTATATCAGA		
		_	GACTGTTATCCATTTTGTTATTATGAAAGTAT		
			AAAACAAAACTACTGGAATATAAGACTGCTT		
			CIACAAI GGAAAAI GGI GAAGAGTCTGTGAA		
			GCTGCTGCCACCTCAAAACTTGTGCCAAAA		
			CTATAGCATATCCACATGTTGTAAGAACAAGA		
			CTACGTGAAGAGGGAACAAAATACAGATCTT		
			TTTTCAGACTCTATCTTTGCTTGTTCAAGAA		
-			GAAGGTTATGGGTCTCTTTATCGTGGTCTGA		
			CAACTCATCTAGTGAGACAGATTCCAAACACA		
			GCCATTATGATGGCCACCTATGATTGGTGG		
ď	V090,00	5	11 ACCIACICAAI GGAI AG		
	preyzos4	701		53	MAHAMENSWTISKEYHIDEEV
0.5			CAG AAAGAGTACCATATTGATGAAGAGTG		GFALPNPOENLPDFYNDWMFI
			GGCTTTGCTCTGCCAAATCCACAGGAAAATC		AKHLPDLIESGOLRERVEKI N
			TACCTGATTTTTATAATGACTGGATGTTCATT		MLSIDHLTDHKSORLARLVI G
			GCTAAACATCTGCCTGATCTCATAGAGTCTG		CITMAY/WGKGHGDVRKVI P
_			GCCAGCTTCGAGAAGAGTTGAGAAGTTAAA		RNIAVPYCOI SKKI FI PPII VY
			CATGCTCAGCATTGATCATCTCACAGACCAC		ADCVLANWKKKDPNKPLTYF
			AAGTCACAGCGCCTTGCACGTCTAGTTCTGG		NMDVLFSFRDGDCSKGFFLVS
			GATGCATCACCATGGCATATGTGTGGGGCAA		LLVEIAAASAIKVIPTVEKAMOM
			AGGTCATGGAGATGTCCGTAAGGTCTTGCCA		QERDTLLKALLEIASCI FKAI O
			AGAAATATTGCTGTTCCTTACTGCCAACTCTC		VEHOIHDHVN
			CAAGAAACTGGAACTGCCTCCTATTTTGGTTT		
			ATGCAGACTGTGTCTTGGCAAACTGGAAGAA		
			AAAGGATCCTAATAAGCCCCTGACTTATGAG		
			AACATGGACGTTTTGTTCTCATTTCGTGATGG		
			AGACTGCAGTAAAGGATTCTTCCTGGTCTCT		
			CTATTGGTGGAAATAGCAGCTGCTTCTGCAA		
			TCAAAGTAATTCCTACTGTATTCAAGGCAATG		

				CAAATGCAAGAACGGGACACTTTGCTAAAGG CGCTGTTGGAAATAGCTTCTTGCTTGGAGAA AGCCCTTCAAGTGTTTCACCAAATCCACGATC		
Shigella ipa H9.8	g.	prey67740	153	GNATGNATTACNTGCNATANTGTAGAAATTG GGCATGNGGACAAGGGGATGGTTCATGTATC TCTTAACTGTCTGACATGGNAACATNGTCTAT ACCNAGTTNGNGTGCACTTTTAAAATGAATCC GATTTGTCTGCACTNNNNTNCCNCNTCTNCC TCNTTNTATGTGNGTGCAGCGTTTACNCTACT NCANTCTGANTGTACTTANTGGTNATCTTNCN TGCNNTTGNGGNGANGGGGGGN	354	XXITCXXVEIGHXDKGMVHVS LINCLTWXHXLYXVXVHF*NES DLSALXXXXXLXXCXCSVYXT XX*XYLXVIXXAXXXGXGXRXF XLCTXXGG
Shigella ipaH9.8	ဖ	prey67703	154	0747050000000404	355	AIEKLLALLNTLDRWIDETPPV DQPSRFGNKAYRTWYAKLDE EAENLVATVVPTHLAAAVPEV AVYLKESVGNSTRIDYGTGHE AAFAAFLCCLCKIGVLRVDDQI AIVFKVFNRYLEVMRKLQKTY RMEPAGSQGVWGLDDFQFLP FIWGSSQLIDH
Shigella ipaH9.8	ဖ	prey67741	155	GACAAGTTGAGCCAAGCAAAAGCCTACTGCA 3 ACTTGGGCCTAGCATTCAAGGCTCTGCTGAA TTTCAGTAAAGCTGAAGAGTGTCANGAAGTA CCTACTGTCCCTAGCCCAGTCTCTGAATAATT CCCAGGCTAAATTTCGAGCCCTAGGAAACCT GGGCGATATATTCATCTGTAAAAAAAAAGATAAA	356	DKLSQAKAYCNLGLAFKALLN FSKAEECXEVPTVPSPVSE*FP G*ISSPRKPGRYIHL*KRYKWC NKIL*AATGLSSPGKGQKIRSQ CICSP

			_	ATGGTGCAATAAAATTCTATGAGCAGCAACTG		
•				GGCTTAGCTCACCAGGTAAAGGACAGAAGAT		
				\neg		
Shigella	ဖ	prey67742	156	AGGTAATGGAGCTGGTGGCAGCAGCCA	357	GNGAGGGSSQKTPLFETYSD
раН9.8				GAAAACTCCACTCTTTGAAACTTACTCGGATT		WDREIKRTGASGWRVCSINE
				GGGACAGAGAATCAAGAGGACAGGTGCTTC		GYMISTCLPEYIVVPSSLADQD
				CGGGTGGAGAGTTTGTTCTATTAACGAGGGT		LKIFSHSFVGRRMPLWCWSH
				TACATGATATCCACTTGCCTTCCAGAATACAT		SNGSALVRMALIKDVLQQRKI
				TGTAGTGCCAAGTTCTTTAGCAGACCAAGAT		DQRICNAITKSHPQRSDVYKS
				CTAAAGATCTTTTCCCATTCTTTTGTTGGGAG		DLDKTLPNIQEVQAAFVKLKQL
				AAGGATGCCACTCTGGTGCTGGAGCCACTCT		CVNEPFEETEEKWLSSLENTR
				AACGGCAGTGCTCTTGTGCGAATGGCCCTCA		WLEYVRAFLKHSAELVYMLES
				TCAAAGACGTGCTGCAGCAGAGGAAGATTGA		KHLSVVLQEEEGRDLSCCVAS
				CCAGAGGATTTGTAATGCAATAACTAAAAGTC		LVQVMLDPYFRTITGFQSLIQK
		***		ACCCACAGAGAGGGATGTTTACAAATCAGAT		EWVMAGYQFLDRCNHLKRSE
				TTGGATAAGACCTTGCCTAATATTCAAGAAGT		KESPLFLLFLDATWQLLEQYP
				ACAAGCAGCATTTGTAAAACTGAAGCAGCTAT		AAFEFSETYLAVLYDSTRISLF
				GCGTTAATGAGCCTTTTGAAGAAACTGAAGA		GTFLFNSPHQRVKQSTVSRIK
				GAAATGGTTATCTTCACTGGAAAATACTCGAT		SCTKQDYFPSRV*
				GGTTAGAATATGTAAGGGCATTCCTTAAGCAT		
				TCAGCAGAACTTGTATACATGCTAGAAAGCAA		
				ACATCTCTGTAGTCCTACAAGAGGAGAA		
				GGAAGACTTGAGCTGTTGTGTAGCTTCTC		
				TTGTTCAAGTGATGCTGGATCCCTATTTAGG		
				ACAATTACTGGATTTCAGAGTCTGATACAGAA		
				GGAGTGGGTCATGGCAGGATATCAGTTTCTA		
				GACAGATGCAACCATCTAAAGAGATCAGAGA		
		•		AAGAGTCTCCTTTATTTTTGCTATTCTTGGAT		
-				GCCACCTGGCAGCTGTTAGAACAATATCCTG		
				CAGCTTTTGAGTTCTCCGAAACCTACCTGGC		
				AGTGTTGTATGACAGCACCCGGATCTCACTG		
				TTTGGCACCTTCCTGTTCAACTCCCCTCACCA		
				GCGAGTGAAGCAAGCACGGTCAGTAGGATA		
				AAAAGTTGTACAAAACAAGATTATTTCCTTC		
				ACGAGILIGA		

	158	1	prey67337	6 prey67337
KE S A S E S E	AGCTGCACCCAGATGATGTGGCAGGGATCCA GGCTCTCTATGGCAAGAAGAGTCCAGTGATA AGGGATGAGGAAGAAGAGAGCAGAGC	9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	A 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	A 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

				GAGTGACATGGGACTTCAGCATGAGCAATGG AGGGCCCCGTGGAAGACCTATGCTTTCAAG		
				GGGGACTATGTGGGACTGTATCAGATTCAG		
				GACCEGECCCI GI CCGAG GI CI GCCCI TTGGGAGGGGCTCCCGGAAACCTGGATGC		
			·	TGCTGTCTACTCGCCTCGAACACAATGGATT		
Shigella	9	prey67746	159	+	0	MEKYSIMKSMNMHRKKGKRT
ipaH9.8				TATGCATCGAAAAAAGGAAAAAGGACCATTT		LEMTQILKRHGYCTLGEAFNR
				TAGAAATGACACAAATACTCAAAAGGCATGG		LDFSSAIQDIRTFNYVVKLLQL
				CTATTGCACCTTGGGAGAGGCCTTTAATCGG		AKSQLTSLSGVAQKNYFNILD
				TTAGACTTCTCAAGTGCAATTCAAGATATCCG		KIVOKVLDDHHNPRLIKDLLQD
				AACGTTCAATTATGTGGTCAAACTGTTGCAGC		LSSTLCILIRGVGKSVLVGNINI
				TAATTGCAAAATCCCAGTTAACTTCATTGAGT		WICRLETILAWQQQLQDLQMT
				GGCGTGGCACAGAAGAATTACTTCAACATTTT		KOVNNGLTLSDLPLHMLNNILY
	. ,			GGATAAAATCGTTCAAAAGGTTCTTGATGACC		RFSDGWDIITLGQVTPTLYMLS
				ACCACAATCCTCGCTTAATCAAAGATCTTCTG		EDROLWKKLCQYHFAEKQFC
				CAAGACCTAAGCTCTACCCTCTGCATTCTTAT		RHLILSEKGHIEWKLMYFALOK
				TAGAGGAGTAGGGAAGTCTGTATTAGTGGGA		HYPAKEQYGDTLHFCRHCSIL
				AACATCAATATTTGGATTTGCCGATTAGAAAC		FWKDSGHPCTAADPDSCFTP
				TATTCTCGCCTGGCAACAACAGCTACAGGAT		VSPQHFIDLFKF*
				CTTCAGATGACTAAGCAAGTGAACAATGGCC		
				TCACCCTCAGTGACCTTCCTCTGCACATGCT		
				GAACAACATCCTATACCGGTTCTCAGACGGA	_	
				TGGGACATCATCACCTTAGGCCAGGTGACCC		
				CCACGITGTATATGCTTAGTGAAGACAGACA		
				GCTGTGGAAGAAGCTTTGTCAGTACCATTTT		
				GCTGAAAAGCAGTTTTGTAGACATTTGATCCT		
		-		TTCAGAAAAAGGTCATATTGAATGGAAGTTGA		
				TGTACTTTGCACTTCAGAAACATTACCCAGCG		
				AAGGAGCAGTACGGAGACACACTGCATTTCT		
				GTCGGCACTGCAGCATTCTCTTTTGGAAGGA		
				CTCAGGACACCCCTGCACGGCGGCCGACCC		
				TGACAGCTGCTTCACGCCTGTGTCTCCGCAG		
				CACTICATCGACCTCTTCAAGTTTTAA		

Shigella ipaH9.8	9	prey54430	160	GCTGTCCAAAACCAACAGGACCCTCTTTATAT TTGGTGTCACAAAGTATATTGCAGGACCCTAT	361	LSKTNRTLFIFGVTKYIAGPYE CEIRNPVSASRSDPVTLNLLH
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				GAATGTGAAATACGGAACCCAGTGAGTGCCA GCCGCAGTGACCCAGTCACCTGAATCTCCT		GPDLPSIYPSFTYYRSGENLYL SCFAESNPRAQYSWTINGKFO
				CCATGGTCCAGACCTCCCCAGCATTTACCCT		LSGOKLSIPQITTKHSGLYACS
				TCATTCACCTTTACCGTTCAGGAGAAACCT		VRNSATGKESSKSITVKVSDW
				CLACITGICCTGCTTCGCCGAGTCTAACCCA		ILP*
				AGTTTCACCTATCACCACAAIIAAIIGGGA		
				CCCCAAATAACTACAAAAAAAAAAAAAAAAAAAAAAAA		
				ATGCTTGCTCTGTTCGTAGTCAGCCACTGG		
				CAAGGAAAGCTCCAAATCCATCACAGTCAAA		
				GTCTCTGACTGGATATTACCCTGA		
Shigella	9	prey67749	161	AAGAAATTTAAGTATATTGAGAATTTGGAAAA	362	KKFKYIENLEKCVKLEVLNLSY
ipaH9.8				ATGTGTTAAACTTGAAGTACTGAATCTCAGCT		NLIGKIEKLDKLLKLRELNLSYN
				ATAATCTAATAGGGAAGATTGAAAAGTTGGAC		KISKIEGIENMCNLQKLNLAGN
				AAGCTGTTAAAATTACGTGAACTCAACTTATC		EIEHIPVWLGKKLKSLRVL
				ATATAACAAAATCAGCAAAATTGAAGGCATAG		
				AAAATATGTGTAATCTGCAAAAGCTTAACCTT		
				GCAGGAAATGAATTGAGCATATTCCAGTAT		
				GGTTAGGGAAGAGTTAAAATCTTTGCGAGT		
Shigella	9	prey67751	162	GGAGGCAGAGACACTGTCTTAAAAA	363	GGRARHCLLKKGKKTRQES*
ран9.8	_			AAGGAAAGAAACTCGACAAGAATCCTAGTG		WERQDHPVMGQ**PSHGAQ*
				GGAGAGGACCATCCTGTGATGGGTCA		CRKRGCECQEGQFRTTWQG
				ATAATGACCCAGTCATGGAGCACAGTGATGC		KQACENGPSEPELREELSLGL
				AGGAAAAGGGGTTGTGAGTGCCAGGAAGGC		SGGAVFXVG
				CAGTTTCGAACAACGTGGCAAGGGAAGCAG		
				GCCTGTGAGAACGGGCCCTCTGAGCCGGAA		
				CTGAGGGAGGTTGAGCCTGGGGCTCTCT		
				GGGGGTGCAGTGTTCCANGTGGGGGA		
Shigella	ဖ	prey8739	163	_	364	AEPPVPSPLPLASSPESARPK
ipaH9.8				CTGGCCTCATCCCCTGAATCAGCCCGACCCA	•	PRARPPEEGEDTRPPRLKKW
				AGCCCCGTGCCCGGCCCCTGAAGAAGGTG		KGVRWKRLRLLTIQKGSGRQ
				AAGATACCCGTCCTCGCCTCAAGAAATG		EDEREVAEFMEGLGTALRPDK

				GAAAGGAGTGCGCTGGAAGCGGCTTCGGCT GCTGCTGACCATCCAGAAGGGCAGTGGACG		VPRDMRRCCFCHEEGDGATD GPARLINLDLDLWWHLNCALW
				GCAGGAGGAGGGGGGAAGTGGCAGGTT		STEVYETQGGALMNVEVALH
				GACAAGGTACCGCGAGACATGCGTCGCTGC		MRCPNVYHFGCAIRAKCMFFK
				TGTTTCTGTCATGAGGAGGGTGACGGGGCCA		DKTMLCPMHKIKGPCEQELSS
				CTGATGGGCCTGCCGTCTGCTGAACCTGGA		FAVERR
				CCTGGACCTGTGGGTGCACCTCAACTGTGCC		
				CTTTGGTCCACGGAGGTGTATGAGACCCAGG		
•				GCGGAGCACIGAIGAAIGIGGAGGTIGCCCT		
				GCACCGAGGACTGCTAACCAAGTGCTCCCTG		
				TGCCAGCGAACTGGTGCCACCAGCAGCTGC		
				AATCGCATGCGTTGCCCCAATGTCTACCATTT		
				TGGTTGTGCCATCCGCGCCAAGTGCATGTTC		
				TTCAAGGACAAGACCATGCTGTGTCCAATGC		
				ATAAGATCAAGGGGCCCTGTGAGCAAGAGCT		
				GAGCTCTTTTGCTGTCTTCCGGCGGG		
Shigella	9	prey18232	164	_	365	SDMMLNIINSSITTKAISRWSSL
ipaH9.8				CTATTACTACCAAAGCCATCAGCCGGTGGTC		ACNIALDAVKMVQFEENGRKE
				ATCTTTGGCTTGCAACATTGCCCTGGATGCT		IDIKKYARVEKIPGGIIEDSCVL
				GTCAAGATGGTACAGTTTGAGGAGAATGGTC		RGVMINKDVTHPRMRRYIKNP
				GGAAAGAGATTGACATAAAAAAATATGCAAGA		RIVLLDSSLEYKKGGSQTDIEIT
				GTGGAAAAGATACCTGGAGGCATCATTGAAG		REEDFTRILAMEEEYIQQLCE
				ACTCCTGTGTCTTGCGTGGAGTCATGATTAA		DIIQLKPDVVITEKGISDLAQHY
				CAAGGATGTGACCCATCCACGTATGCGGCGC		LMRANITAIRRVRKTDNNRIAR
				TATATCAAGAACCCTCGCATTGTGCTGCTGG		ACGARIVSRPEELREDDVGTG
				ATTCTTCTCTGGAATACAAGAAAGGAGGAAG		AGLLEIKKIGDEYFTFITDCKDP
				CCAGACTGACATTGAGATTACACGAGAGGAG		*
				GACTTCACCCGAATTCTCCAGATGGAGGAAG		
-				AGTACATCCAGCAGCTCTGTGAGGACATTAT		
				CCAACTGAAGCCCGATGTGGTCATCACTGAA		
-				AAGGGCATCTCAGATTTAGCTCAGCACTACC		
				TTATGCGGGCCAATATCACAGCCATCCGCAG		
				AGTCCGGAAGACAGACAATAATCGCATTGCT		
				AGAGCCTGTGGGGCCCGGATAGTCAGCCGA		

				CCAGAGGAACTGAGAGAAGATGATGTTGGAA	
				CAGGAGCAGGCCTGTTGGAAATCAAGAAAAT	
				TGGAGATGATACTTTACTTTCATCACTGACT GCAAAGACCCCAAGGC	
Shigella	9	prey66739	165	+	 MDDKEI IEYEKSOMKEDPDMA
ipaH9.8					SAVAAIRTLLEFLKRDKGETIO
				TCAGCAGTGGCTGCCATCCGGACGTTGCTG	GLRANLTSAIETLCGVDSSVAV
				GAGTTCTTGAAGAGAGATAAAGGGGAGACAA	SSGGELFLRFISLASLEYSDYS
				TCCAGGGTCTGAGGGCGAATCTCACCAGTGC	KCKKIMIERGELFLRRISLSRN
				CATAGAAACCCTGTGTGGTGTGGACTCCTCT	KIADLCHTFIKDGATILTHAYSR
				GTGGCAGTGTCCTCTGGCGGGGGGGCTCTTC	WLRVLEAAVAAKKRFSVYVT
				CTCCGCTTCATCAGTCTTGCCTCCCTGGAAT	ESOPDLSGKKMAKALCHLNVP
				ACTCCGATTACTCCAAATGTAAAAAGATCATG	VTVVLDAAVGYIMEKADLVIVG
	-			ATTGAGCGGGGAGACTTTTCTCAGGAGAA	AEGVVENGGIINKIGTNOMAV
				TATCACTGTCAAGAACAAAATTGCAGATCTG	CAKAONKPFYVVAESFKFVRL
				TGCCATACTTTCATCAAAGATGGAGCGACAAT	FPLNQQDVPDKFKYKADTLKV
				ATTGACTCACGCCTACTCCAGAGTGGTCCTG	AQTGODLKEEHPWVDYTAPS
				AGAGTCCTGGAAGCAGCCGTGGCGGCCAAG	LITLLFTDL
				AAGCGATTTAGTGTATACGTCACAGAGTCAC	
				AGCCTGATTTGTCAGGTAAGAAAATGGCCAA	
				AGCCCTCTGCCACCTCAACGTCCCTGTCACT	
				GTGGTGCTAGATGCTGCTGTCGGCTACATCA	
				TGGAGAAAGCAGATCTTGTCATAGTTGGTGC	
	_			TGAAGGAGTTGTTGAAAACGGAGGAATTATT	
				AACAAGATTGGAACCAACCAGATGGCTGTGT	
				GTGCCAAAGCACAGAACAAACCTTTCTATGT	
				GGTTGCAGAAAGTTTCAAGTTTGTCCGGCTC	
				TTTCCACTAAACCAGCAAGACGTCCCAGATA	
				AGTTTAAGTATAAGGCAGACACTCTCAAGGT	
_				CGCGCAGACTGGACAAGACCTCAAAGAGGA	
				GCATCCGTGGGTCGACTACACTGCCCCTTCC	
Shigella	ဖ	prey67769	166	_	AAFKVATPYSLYVCPEGQNVT
рану.8				TGTATGTCTGTCCCGAGGGGCAGAACGTCAC	LTCRLLGPVDKGHDVTFYKTW
				CCTCACCTGCAGGCTCTTGGGCCCTGTGGAC	YRSSRGEVOTCSERRPIRNLT

FQDLHLHHGGHQAANTSHDL AQRHGLESASDHHGNFSITMR NLTLLDSGLYCCLVVEIRHHHS EHRVHGAMELQVQTGKDAPS NCVVYPSSSQDSENITAAALA TGACIVGILCLPLILLLVYKQRQ AAS	LGAGPFSHMIKLKTKPLPPDP PRLECVAFSHQNLKLKWGEG TPKTLSTDSIQYHLQMEDKNG RFVSLYRGPCHTYKVQRLNES TSYKFCIQACNEAGEGPLSQE YIFTTPKSVPAALKAPKIEKVN DHICEITWECLQPMKGDPVIYS LQVMLGKDSEFKQIYKGPDSS FRYSSLQLNCEYRFRVCAIR
	368 8
	CCTTGGAGCTGGTCCTTTCAGCCATATGATA AAATTAAAAACTAAGCCTCTCCCTCCTGATCC ACCTCGTCTGGAATGTGTTGCCTTTTAGCCAC CAGAACCTTAAGCTGAAATGGGGAGAAGGAA CTCCAAAGACATTGTCAAACGGATTCTATTCAG TACCACCTTCAGATGGAGGATAGAAGGAACGTTGTATCAGATGAAGAATGAAGAATGAAAATTCTGTAATCAAGAGGACCATGTCATAATGAAAATTCTGTAATCAAGAGGACCATGTCATAAATTCCTATAAATTCTGTAATCAAGAGGTCCCCTCTCCCAAGAATAATTCCTAAAAATTCTGTAATTCACTAAAATTCTGTAAAATTCTGTAAAAATTCTGTAAAATTCTGTAAAATTCTGTAAAATTCTGTAAAAATTCTGTAAAAATTCTGTAAAAAAAA
	167
	prey13613
	Φ
	Shigella ipaH9.8

preyood	8	GGCTCGGCTGAAGGACCTGGAGTGACTGCT	369	ARLKOLEALLNSKEAALSTALS
		TCTCAGTGAGAGCGCACGCTGGAGGCCGA		ALGEAKKQLQDEMLRRVDAE
		GCTGCATGATCTGCGGGGCCAGGTGGCCAA		NRLQTMKEELDFQKNIYSEEL
		GCTTGAGGCAGCCCTAGGTGAGGCCAAGAA		RETKRRHETRLVEIDNGKQRE
		GCAACTTCAGGATGAGATGCTGCGGCGGGT		FESRLADALQELRAQHEDQVE
		GGATGCTGAGAACAGGCTGCAGACCATGAA		QYKKELEKTYSAKLDNARQSA
		GGAGGAACTGGACTTCCAGAAGAACATCTAC		ERNSNLVGAAHEELQQSRIRI
		AGTGAGGAGCTGCGTGAGACCAAGCGCCGT		DSLSAQLSQLQKQLAAKEAKL
		CATGAGACCCGACTGGTGGAGATTGACAATG		RDLEDSLARERDTSRRLLAEK
		GGAAGCAGCGTGAGTTTGAGAGCCGGCTGG		EREMAEMRARMQQQLDEYQ
		CGGATGCGCTGCAGGAACTGCGGGCCCAGC		ELLDIKLALDMEIHAYRKLLEG
		ATGAGGACCAGGTGGAGCAGTATAAGAAGGA		EEERLRLSPSPTSQRSRGRAS
		GCTGGAGAGACTTATTCTGCCAAGCTGGAC		SHSSQTQGGGSVTKKRKLES
		AATGCCAGGCAGTCTGCTGAGAGGGAACAGCA		TESRSSFSQHARTSGRVAVEE
		ACCTGGTGGGGGCTGCCCACGAGGAGCTGC		VDEEGKFVRLRNKSNEDQSM
		AGCAGTCGCGCATCGCATCGACAGCCTCTC		GNWQIKRONGDDPLLTYRFP
		TGCCCAGCTCAGCCAGCTCCAGAAGCAGCT		PKFTLKAGQWTIWAAGAGAT
		GGCAGCCAAGGAGGCGAAGCTTCGAGACCT		HSPPTDLVWKAQNTWGCGNS
-		GGAGGACTCACTGGCCCGTGAGCGGGACAC		LRTALINSTGEEVAMRKLVRS
		CAGCCGGCGGCTGCTGGCGGAAAAGGAGCG		VTVVEDDEDEDGDDLLHHHH
		GGAGATGGCCGAGATGCGGGCAAGGATGCA		VSGSRR*
		GCAGCAGCTGGACGAGTACCAGGAGCTTCT		
		GGACATCAAGCTGGCCCTGGACATGGAGATC		
		CACGCCTACCGCAAGCTCTTGGAGGGCGAG		
		GAGGAGGCTACGCCTGTCCCCCAGCCCT		
		ACCTCGCAGCGCAGCCGTGGCCGTGCTTCC		
		TCTCACTCATCCCAGACACAGGGTGGGGGCA		
		GCGTCACCAAAAGCGCAAACTGGAGTCCAC		
		TGAGAGCCGCAGCAGCTTCTCACAGCACGCA		
		CGCACTAGCGGGCGCGTGGCCGTGGAGGAG		
		GTGGATGAGGAGGCCAAGTTTGTCCGGCTG		_
_		CGCAACAAGTCCAATGAGGACCAGTCCATGG		
		GCAATTGGCAGATCAAGCGCCAGAATGGAGA		
		TGATCCCTTGCTGACTTACCGGTTCCCACCA		

				ACGATCTGGGCTGCAGGAGCTGGGGGCCACC CACAGCCCCCTACCGACCTGGTGGAAG		
				GCACAGAACACCTGGGGCTGCGGGAACAGC		
				CIECUI ACECCI CI CALICACI CCACI GGGG		
_				CAGTGACTGTGGTTGAGGACGACGAGGATG		
	_			AGGATGGAGATGACCTGCTCCATCACCACCA		
Shigella	9	prey67774	169	CCCACCTCCTGGCCGGTCCTTGAAGTTTTCT	370	PPPGRSLKFSGVYGPIICORP
ipaH9.8				()		STNELPLEDEPVKEVEELIGVE
				CAAGTACCAATGAGCTTCCCCTATTTGACTTT		NVFQLFTCALLEFQILLYSOHY
				CCTGTCAAAGAGGTTTTTGAACTGCTCGGGG		QRLMTVAETITALMFPFQWQH
				TGGAGAATGTGTTTCAGCTTTTTACTTGTGCC		VYVPILPASLLHFLDAPVPYLM
				CTTCTGGAGTTTCAAATCCTGCTCTACTCACA		GLHSNGLDDRSKLELPQEANL
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				ACGATTACAGCTCTCATGTTTCCTTTCCAGTG		LEFVQEVSEILMAFGIPPEGNL
				GCAGCATGTCTATGTCCCTATTCTCCCAGCTT		HCSESASKLKRLRASELVSDK
				CTCTCCTGCATTTCTTAGATGCTCCTGTTCCA		RNGNIAGSPLHSYELLKENETI
				TACCTGATGGGTTTGCATTCCAATGGCCTGG		ARLOALVKRTGVSLEKLEVRE
				ATGACCGGTCAAAGCTGGAGCTGCCTCAAGA		DPSSNKDLKVQCDEEELRIYQ
				GGCTAACCTCTGCTTTGTGGACATTGACAAC		LNIQIREVFANRFTQMFADYEV
				CACTICATTGAGTTGCCAGAGGACTTGCCAC		FVIQPSQDKESWFTNREQMQ
				AGTTCCCCAACAATTGGAGTTTGTCCAGGA		NFDKASFLSDQPEPYLPFLSR
				AGTCTCTGAGATTCTCATGGCATTTGGAATTC		FLETQMFASFIDNKIMCHDDD
				CCCCTGAAGGGAATCTTCATTGCAGTGAGAG		DKDPVLRVFDSRVDKIRLLNV
				TGCCTCCAAGCTGAAGAGGCTGCGGGCCTC		RTPTLRTSMYQKCTTVDEAEK
				IGAGCTTGTCTCGGACAAGAGGAATGGGAAC		AIELRLAKIDHTAIHPHLLDMKI
				Allecieeciccctifecattcctaceaec		GGGKYEPGFFPKLQSDVLST
				TTCTTAAGGAGAATGAAACTATTGCCCGGCT		GPASNKWTKRNAPAQWRRK
				GCAAGCCTTGGTCAAGAGAACTGGGGTGAG		DRAKAHTEHLRLDNDAREKYI
				CCTGGAAAAGTTGGAAGTGCGTGAAGACCCC		QEARTMGSTIRQ
		-		AGCAGCAATAAGGATCTCAAAGTTCAGTGTG		
				ATGAAGAAGACTCAGGATTTACCAGCTAAA		
				CATTCAGATCCGGGAAGTTTTTGCAAATCGTT		
				TCACTCAGATGTTTGCAGATTATGAGGTGTTT		

	_			GTCATCCAACCCAGCCAGGATAAGGAATCCT		
				GGTTTACCAACAGGGAGCAAATGCAAAACTT		
				TGATAAAGCATCTTTTCTGTCAGATCAGCCTG		
				AGCCCTACCTGCCCTTCCTCAAGATTCCT		
				GGAGACCCAGATGTTTGCATTCATTGACA		
				ACAAAATAATGTGTCATGATGATGATGATAAA		
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				TTGACAAGATCAGGCTGTTGAATGTTCGGAC		
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				GTACCACTGTGGATGAAGCAGAGAAAGCAAT		
				TGAGCTGCGTCTGGCAAAAATTGACCATACT		
				GCAATTCACCCACATTTACTTGACATGAAGAT		
				TGGACAAGGGAAATATGAGCCGGGCTTCTTC		
				CCTAAGCTGCAGTCTGATGTACTTTCCACTG		
				GGCCAGCCAGCAACAGTGGACGAAAAGGA		
				ATGCCCCTGCCCAGTGGAGGCGGAAAGATC		
				GGCAGAAGCAGCACACAGAACACCTGCGTTT		
				AGATAATGACCAGAGGAGAGAGTACATCCAG		
				GAAGCCAGGACTATGGGCAGCACTATCCGC		
:				CAG		
Shigella	ဖ	prey67776	170		371	WDSTKISKAYYKAMVISTWCY
ipa⊓3.0				CAAAGCAAIGGIAATTAGCACTTGGTGTTACT		WLRKRHLMHETDSRVPVSLLF
				GGCTAAGAAAGAGGCACTTGATGCATGAAAC		DTSAISNQQGNWANLLSILKTY
				AGACTCACGTGTACCTGTGAGTTTATTATTTG		XV*XLXDNVLXNGWEVDXXCG
			_	ATACAAGTGCCATTTCAAATCAGCAAGGGAAT		CXAVXA
				IGGGCCAATTTGTTATCCATTTTGAAAACATA		
				TNAAGTTTGATNCCTACNTGACAACGTNCTNT		
				NAAATGGGTGGGAGGTGGATNGGNCATGTG		
				GETETNANGCGGTGNNGGCGG		
Shigella	9	prey4758	171	ပ	372	LSALESTVPPSQPPPVGTSAIH
рану.8				AGCCAGCCTCCACCTGTGGGCACCTCAGCC		MSLLEMRRSVAELRLOLOOM
				ATCCACATGAGCCTGCTTGAGATGAGGCGGA		ROLOLONOELLRAMMKKAFL
				GCGTGGCGGAACTCAGGCTCCAGCTCCAGC		EISGKVMETMKRLEDPVORO
				AGATGCGGCAGCTCCAGCTGCAGAACCAGG		RVLVEQEROKYLHEEEKIVKK
				AGTTGCTGAGGGCAATGATGAAGAAGGCCGA		LCELEDFVEDLKKDSTAASRL

			_	GCTGGAAATCAGTGGCAAAGTGATGGAAACA	VTLKDVEDGAFLIBOVGEAVA
			_	ATGAAGAGACTGGAGGATCCCGTGCAGCGA	TLKGEFPTLONKMRAILRIEVE
				CAGCGCGTCCTAGTGGAGCAAGAGACAA	AVRFLKEEPHKLDSLLKRVRS
				AAATATCTTCATGAGGAAGAGAAGATCGTCAA	MTDVLTMLRRHVTDGLLKGTD
				GAAGTTGTGCGAGTTGGAAGACTTTGTTGAA	AAQAAQYMAMEKATAAEVI K
				GACTTGAAGAAGGACTCCACGGCAGCCAGC	SOEEAAHTSGOPFHSTGAPG
				CGATTGGTTACTCTGAAAGACGTGGAAGACG	DAKSEVVPLSGMMVRHAOSS
				GGGCTTTCCTCCTGCGTCAAGTGGGAGAGG	PVVIQPSQHSVALL NPAONLP
				CTGTAGCTACCCTGAAAGGAGAATTTCCAAC	HVASSPAV
				CTTACAAAACAAGATGCGAGCCATCCTGCGC	
		_		ATAGAAGTGGAGGCCGTGCGGTTTCTGAAGG	
				AGGAGCCACACAAGCTGGACAGTCTCCTGAA	
				GCGTGTGCGCAGCATGACAGACGTCCTGAC	
				CATGCTGCGGAGACATGTCACTGATGGGCTC	
	•	_		CTGAAAGGCACGGACGCAGCCCAAGCCGCA	
				CAGTACATGGCTATGGAAAAGGCCACAGCCG	
				CAGAAGTCCTGAAGAGTCAGGAGGAGGCAG	
_				CCCACACCTCCGGCCAGCCCTTCCACAGCAC	
				AGGTGCCCTGGCGATGCGAAGTCGGAAGT	
				GGTGCCTTTGTCCGGCATGATGGTTCGCCAC	
				GCGCAGAGCTCCCCTGTGGTCATCCAGCCCT	
				CCCAGCACTCCGTGGCCTGCTGAACCCTG	
				CTCAGAACTTGCCTCACGTGGCCAGCTCCCC	
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Shigella	ဖ	prey67781	172	_	 LRTNHIGWVQEFLNEENRGLD
pars.8				GGAGTTCCTCAATGAAGAGAACCGTGGCCTG	VLLEYLAFAQCSVTYDMESTD
				GATGTGCTGCTCGAGTACCTGGCCTTTGCCC	NGASNSEKNKPLEQSVEDLSK
				AGTGCTCTGTCACGTATGACATGGAGAGCAC	GPPSSVPKSRHLTIKLTPAHSR
				AGACAACGGGGCTTCCAACTCAGAGAAAAC	KALR
		_		AAGCCCCTGGAGCAGTCTGTGGAAGACCTCA	i
				GCAAGGGTCCACCCTCCGTGCCCAAAAG	
				CCGCCACCTGACCATCAAGCTGACCCCAGCC	
				$\overline{}$	
Shigella ipaH9.8	9	prey2109	173	GACTAAGGATCACCATTACTTTAAGTACTGCA 374	TKDHHYFKYCKISALALLKMV
				ANTICIONACATIGACIO I CIGANGAI GGI	MHARSGGNLEVMGLMLGKVD

			<u></u>	GATGCATGCCAGATCGGGAGGCAATTTGGAA GTGATGGGTCTGATGCTAGGAAAGGTGGATG		GETMIIMDSFALPVEGTETRVN AOAAAVEVMAAVIENIAKOVCE
				GTGAAACCATGATCATTATGGACAGTTTTGCT		LENAIGWYHSHPGYGCWLSGI
				TTGCCTGTGGAGGGCACTGAAACCCGAGTAA		DVSTQMLNQQFQEPFVAVVID
				ATGCTCAGGCTGCTGCATATGAATACATGGC		PTRTISAGKVNLGAFRTYPKG
				TGCATACATAGAAATGCAAAACAGGTTGGC		YKPPDEGPSEYQTIPLNKIEDF
				CGCCTTGAAAATGCAATCGGGTGGTATCATA		GVHCKQYYALEVSYFKSSLDR
				GCCACCCTGGCTATGGCTGCTGGCTTTCTGG		KLLELLWNKYWVNTLSSSSLL
				GATTGATGTTAGTACTCAGATGCTCAATCAGC		N.
				AGTTCCAGGAACCATTTGTAGCAGTGGTGAT		
				TGATCCAACAAGAACAATATCCGCAGGGAAA		
				GTGAATCTTGGCGCCTTTAGGACATACCCAA		
				AGGGCTACAAACCTCCTGATGAAGGACCTTC		
				TGAGTACCAGACTATTCCACTTAATAAAATAG		
				AAGATTTTGGTGTACACTGCAAACAATATTAT		,
				GCCTTAGAAGTCTCATATTTCAAATCCTCTTT		
				GGATCGCAAATTGCTTGAGCTGTTGTGGAAT		
				AAATACTGGGTGAATACGTTGAGTTCTTCTAG		
				CTTGCTTACTAATGC		
Shigella	9	prey4060	174	_	375	ANHFFFKKDYSKVOHLALHAF
рану.8				GTAAAGTCCAGCATCTGGCCCTCCATGCATT		HNTEVEAMOAESCYOLARSF
				CCATAATACAGAAGTGGAAGCTATGCAAGCA		HVQEDYDQAFOYYYOATOFA
				GAGAGCTGCTATCAGCTAGCTAGATCATTCC		SSSFVLPFFGLGQMYIYRGDK
				ATGTTCAGGAAGATTATGACCAAGCTTTTCAG		ENASOCFEKVLKAYPNNYETM
				TACTATTATCAAGCCACACAGTTTGCCTCATC		KILGSLYAASEDQEKRDIAKGH
				CTCTTTTGTGCTCCCATTTTTGGTTTGGGAC		LKKVTEQYPDDVEAWIELAQIL
				AAATGTATTTATCGAGGTGACAAAGAAAT		EQTDIQGALSAYGTATRILQEK
				GCATCTCAGTGCTTTGAGAAGGTTTTGAAAG		VQADVPPEILNNVGALHFRLG
				CTTATCCTAATAATTACGAAACTATGAAAATTC		NLGEAKKYFLASLDRAKAEAE
				TCGGCTCTCTATGCTGCCTCAGAAGATCA		HDEHYYNAISVTTSYNLARLYE
				AGAAAACGAGATATTGCCAAGGGCCATTTG		AMCEFHEAEKLYKNILREHPN
				AAGAAGGTCACAGAACAGTATCCCGATGATG		YVDCYLRLGAMARDKGNFYE
				TTGAAGCTTGGATTGAATTGGCACAAATCTTA		ASDWFKEALQINQDHPDAWS
				GAACAGACIGATATACAGGGTGCCCTTTCAG		LIGNLHLAKQEWGPGQKKFER
				CCIAIGGAACAGCAACACGAATCCTTCAGGA		ILKQPSTQSDTYSMLALGNVW

		GAAA CTCA	GAAAGTGCAGGCCGATGTTCCTCCAGAGATT CTCAATAATGTGGGTGCCCTCCATTTTAGACT TGGAAACCTAGGGAGCTAAGAAATATTTT	LQTLHQPTRDREKEKRHQDR ALAIYKQVLRNDAKNLYAANGI
		TTG6	TGGCGTCATTGGACCGTGCAAAAGCAGAAG	GAVLAHKGYFKEAKDVFAQV REATADISDVWLNLAHIYVEQK
		200 E	CGGAACACGATGAGCATTACTATAACGCCAT	QYISAVQMYENCLRKFYK
		CTAT	CCG ACCACG CA A A C CGCCAGG CTATATGAGGCGATGTGTGATTCCATGAAG	
		CAGA	CAGAAAAACTGTATAAAAACATCTTACGCGAA	
		CATC	CATCCTAATTATGTTGACTGCTATTTGCGCCT	
_		AGGA	AGGAGCCATGGCTAGAGATAAGGGAAACTTT	
		1 A G	TOAGATTAATCAGGATCATCAGAAGCICI	
		CTT	CTTTGATTGCCAATCTTCATTTGCCAAACAA	
		GAAT	GAATGGGGTCCTGGGCAGAAGAAGTTTGAGA	
-		GGAT	GGATATTAAAACAGCCATCCACACAGAGTGA	
-		TACC	TACCTATTCTATGCTAGCCCTTGGCAACGTGT	
		GGCT	GGCTCCAAACTTTACATCAGCCCACCGAGA	
		TCGA	TCGAGAAAAGGGTCATCAAGATCGT	
		GCTC	GCTCTGGCCATCTACAAACAAGTACTCAGAA	
_		ATGA	ATGATGCAAAGAATCTGTATGCTGCCAATGG	
		CATAC	CATAGGAGCTGTTTTGGCCCACAAAGGATAT	
		SEE -	TTTCGTGAAGCTCGTGATGTATTTGCCCAAGT	
		AAGA	AAGAGAAGCAACAGCAGATATTAGTGATGTG	
		1660	TGGCTGAACTTAGCACACATCTATGTGGAGC	
		AAAA	AAAAGCAGTACATCAGCTTCAGATGTA	
		1	_	
Shigelia 6	prey49284	175 CTCA	CTCATCAACTACGTGGGCTTCATCAACTACCT 376	LINYVGFINYLFYGGTVAGQIV
			OTIONAL GGGGGGCACGGIIGCIGGACAGAIA	LKWKKPUIPKPIKINLLFPIIYLL
		ر اور	GICCIICGCIGGAAGAAGCCIGAIAICCCCC	FWAFLLVFSLWSEPVVCGIGL
		၁၁၁၅	GCCCCATCAAGATCAACCTGCTGTTCCCCAT	AIMLTGVPVYFLGVYWQHKPK
		CATC	CATCTACTTGCTGTTCTGGGCCTTCCTGCTG	CFSDFIELLTLVSQKMCVVVYP
		БТСТ	GTCTTCAGCCTGTGGTCAGAGCCGGTGGTGT	EVERGSGTEEANEDMEEQQQ
		GTGG	GTGGCATTGGCCTGGCCATCATGCTGACAGG	PMYQPTPTKDKDVAGQPQP*
		AGTG	AGTGCCTGTCTATTTCCTGGGTGTTTACTGG	
		CAAC	CAACACAGCCCAAGIGITICAGTGACTTCAT	

			TGAGCTGCTAACCCTGGTGAGCCAGAAGATG TGTGTGGTCGTGTACCCCGAGGTGGAGCGG GGCTCAGGGACAGGAGGCTAATGAGGAC ATGAGGAGCAGCAGCCCATGTACCAA CCCACTCCCACGAGGACAAGGACGTGGCG GGCAGCCCAGGCCCATGTACCAA		
Shigella 6 ipaH9.8	prey67686	176	CTGGGATTACAGGCATGAGCCACAGCACCTG GCTGAGTTTTCTCAGCACCATTTATTGAATAG ACTGTCCTTTCCCTGGTGTATGTTATTGAATAG ACTGTCCTTTCCCTGGTGTATGTTATTGCATT TGTTGAAAATGAGTTCACCATAGATGTGTAGA TTTATTTCTGGGTTCTCTATCCTGTTG GTCTATATGCTTACTGTTTCATGCTGTAGATG CTGTTTTGGTTACTACGGCTCTGTAGTAAAT CTGAAGTCAGGTAATGTGATTCCTCCANTTTT GTTCTTCTGCTNANG	377	LGLQA*ATAPG*VFSAPFIE*TV LSLVYVIAFVENEFTIDV*IYFW VLYPVLLVYMSVFMLVPCCFG YYGSVV*SEVR*CDSSXFVLSA X
Shigella 6 ipaH9.8	prey66872	177	TTTCACTCAAGAAGATATTGACAGAGCTATTG CTTACCTTTCCCAAGTGGTTTGTTTGAGAAA CGAGCCAGGCCAG	378	FTQEDIDRAIAYLFPSGLFEKR ARPVMKHPEQIFPRQRAIQWG EDGRPFHYLFYTGKQSYYSLM ITSFTSRSHRTENS*
Shigella 6 pa H9.8	 prey67690	178	ATGGAGATGAGGCTTCCAGTGGCTCGCAAGC CTCTTAGCGAGAGCTGGGCCGCGCGACATAA GAAACATCTAGTGGTGCCGGGGGGATACAATC ACTACGGACACAGGATTCATGCGGGGGCCATG GAACGTATATGGGAGAAGAAGCTCATTGC ATCTGTTGCTGGCTCTGTGGAGGAGCTCATGC AAGTTGATCTGTGTGAAAGCATCGTAGC AAGTTGATCTGTGAAAGCATCGTAGC GGACGATCACAGAGAGAGAACCAG AAGTTGGTGAAGTAGGAGAGAACTTGCA AGGAATCACAGAGAGGAGAAGATCTGCA GGACGATCACAGAGGAGAGG	379	MEMRLPVARKPLSERLGRDT KKHLVVPGDTITTDTGFMRGH GTYMGEEKLIASVAGSVERVN KLICVKALKTRYIGEVGDIV/G RITERRSAEDELAMRGFLQE GDLISAEVQAVFSDGAVSLHT RSLKYGKLGQGVLVQVSPSLV KRQKTHFHDLPCGASVILGNN GFIWIYPTPEHKEEEAGGFIAN LEPVSLADREVISRLRNCIISLV TQRMMLYDTSILYCYEASLPH QIKDILKPEIMEEIVMETRQRLL

EQEG.	KDLNMNVNSFQRKFVNEVRR CESLERILRFLEDEMQNEIVVQ LLEKSPLTPLPREMITLETVLE KLEGELGEANQNQQALKQSFL ELTELKYLLKKTQDFFETETNL ADDFFTEDTSGLLELKAVPAY MTGKLGFIAGVINRERMASFE RLLWRICRGNVYLKFSEMDAP LEDPVTKEEIQKNIFIIFYQGEQ LRQKIKKICDGFRATVYPCPEP AVEREMLESVNVRLEDLITVI TQTESHRQRLLQEAAANWHS WLIKVQKMKAVYHILNMCNIDV TQQCVIAEIWFPVADATRIKRA LEQGMELSGSSMAPIMTTVQS KTAPPTFNR
- C - 4 - C C	08 0 0 0 0 15 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
CACACGAGGAGCCTGAAATATGGAAAACTAG GTCAGGGGGGTTTTGGTCCAGGTTTCCCCCTC CCTGGTGAAACGGCAGAAGACCCACTTTCAT GATTTGCCATGTGGTGCCTCAGTGATTCTCG GTAACAACGGCTTCATCTGGATTTACCCCACACA CCTGAGCACAAGAAGAGGGAATTACCCAACA CCTGAGCACAAAGAGAGGAACTCTCTTTGC TCATTGCAAACCTGGATATCCCGACACA TGATCGAGAGGTGATATCCCGGCTTCGGAAC TGCTGTATGAACCTGGTAACTCAGAGGATGA TGCTGTATGATACCAGCATCAAAGACA TCTTAAAAGCCAGAATAATGGAGGAGGATGT GATGGAACACCCAGAGGCCTTTTGGAACAG	CAAAGATTTAAATATGAATGTGAACAGCTTTC AAAGGAAATTTGTGAATGAAGTCAGAAGGTG TGAATCACTGGAGAGATCCTCCGTTTTCTG GAAGACGAGATGCAAATGAGATTGTAGTTC GAAGACGAGATGCAAATGAGATTGTAGTTC CCACCGGGAAAAGCCCACTGACCCCGCT CCACCGGGAAATGATTACCCTGAACAAG CCTACAAAAACTGGAAGGAGACTGTT CCAACCAGAACCAGCAGAGCTTTACTGAAAAAG CTTCCTAGAAACGCAGAACTTCTTTACTGAAAAG AACCAATTTAGCTGATGATTCTTTACTGAGG ACCTTCTGGCCTCCTGGAAGTTGAAGGGA AACCAATTTGACCGGAAAGTTGAAGGGA AACCAATTTGACCGGAAAGTTGAAGGGATC ATAGCCGGTGTGATCACGGAAGTTCAGGG ACCTTCCTTTGAGCGGTTACTGGGGATC ATAGCCGGTGTACTTGAAGGGAGGGTG GCTGCATATATGACCGGAAAGTTCAGGG AATAGCAGGAACGTGTACTTGAAGAGGGATC ATAGCCGGTGTACTTGAAGGGAGAGGTC ATAGCCGGTGTACTTGAAGGGAAGTCATCATCATCATCATCAGGAAGAACGTGTACTGGAGGAACCTTGAAGAACATTTCATCA AATCAAGAAACTGTGAAGAACATATTCATCA AATCAAGAAACTTGAAGAACATATTCATCA AATCAAGAAACGTGTGAAGACCTCAGGCCGAAA AATCAAGAAACGTGTGAAGACCTCAGGCCGAAA AATCAAGGAACCTTGCAGACCTGCGGTGG
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	prey67695
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	Shigella ipaH9.8

				AGCGCAGAGATGTTGGAGAGCGTCAATGT GAGGCTGGAAGATTTAATCACCGTCATAACA	
				CAAACAGAGTCTCACCGCCAGCGCCTGCTGC	
				TCATCAAGGTGCAGAAGATGAAAGCTGTCTA	
				ACCCAGCAGTGTCATCGCCGAGATCTGGT	_
				TCCCGGTGGCAGATGCCACGTATCAAGAG	
				CTCCTCCATGGCCCCCATCATGTGGTG	
				CAATCTAAAACAGCCCCTCCCACATTTAACAG	
Shigella	9	prey67336	180	1	MCVTWDESMSNCOBBOVTX
ipaH9.8					AFKGDYVWTVSDSGPGPLFR
				CAAGGGGACTATGTGTGGACTGTATCAGAT	VSALWEGLPGNLDAAVYSPRT
				TCAGGACCGGCCCCTTGTTCCGAGTGTCTG	QWIHFFKGDKVWRYINFKMSP
				CCCTTGGGAGGGCTCCCCGGAAACCTGG	GFPKKLNRVEPNLDAALYWPL
				AIGCIGCIGICTACTCGCCTCGAACACAATG	NQKVFLFKGSGYWQWDELAR
			_	GALICACIICITTAAGGGAGACAAGGTGTGG	TDFSSYPKPIKGLFTGVPNQP
				CGCIACATTACAAGATGTCTCCTGGCTT	SAAMSWQDGRVYFFKGKVY
				CCCCAAGAAGCTGAATAGGGTAGAACCTAAC	WRLNQQLRVEKGYPRNISHN
				CTGGATGCAGCTCTCTATTGGCCTCTCAACC	WMHCRPRTIDTTPSGGNTTP
				AAAAGGTGTTCCTCTTTAAGGGCTCCGGGTA	SGTGITLDTTLSATETTFEY*
				CTGGCAGTGGGACGAGCTAGCCCGAACTGA	
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				CTGCTATGAGTTGGCAAGATGGCCGAGTCTA	
				CTTCTTCAAGGGCAAAGTCTACTGGCGCCTC	
				AACCAGCAGCTTCGAGTAGAGAAAGGCTATC	
				CCAGAAATATTTCCCACAACTGGATGCACTGT	
				CGTCCCCGGACTATAGACACTACCCCATCAG	
				GTGGGAATACCACTCCCTCAGGTACGGGCAT	
				AACCTTGGATACCACTCTCTCAGCCACAGAA	
				-1	
Shigella	9	prey6299	<u>2</u>	AGACCAGAGCCATGTTGTTCAAGAGCATTTA 382	DQSHVVQEHLSEEKDERLHC

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pang.o	AGIGAAGAAAGGATGAAAGACTACACTGTG	ENNDKAPESESEKPTPLSTGO
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	 AGAGAAGCCAACTCCTCTGTCCACTGGGCAA	GPTLKNVMMKNNKI AVSPNY
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Shigella	9	prey6586	182	CGCGCCGTGGAAGATCCAGCAGACAC	383	APWKKIOONTETRWCNEHI K
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				\neg		
	.	prey56789	183		PNIIQFVPADGPLFGDTVTSSE	т
pans.o				GGGCCCTATTGGGGACACTGTCACCAGCT	HLCGINFTGSVPTFKHLWKQV	
	_			CAGAGCACCTCTGTGGCATCAACTTCACAGG	AQNLDRFHTFPRLAGECGGK	
				CAGTGTGCCCACCTTCAAACACCTGTGGAAG	NFHFVHRSADVESVVSGTLRS	
	•			CAGGTGGCCCAGAACCTGGACCGGTTCCAC	AFEYGGGKCSACSRLYVPHSL	
				ACCITCCCACGCCTGGCTGGAGAGTGCGGC	WPQIKGRLLEEHSRIKVGDPA	
				GGAAAGAACTTCCACTTCGTGCACCGCTCGG	EDFGTFFSAVIDAKSFARIKKW	
	_			CCGACGTGGAGAGCGTGAGCGGGACCC	LEHARSSPSLTILAGGKCDDS	
				ICCGCICAGCCTTCGAGTACGGTGGCCAGAA	VGYFVEPCIVESKDPQEPIMK	
				GIGITCCGCCTGCTCGCGTCTCTACGTGCCG	EEIFGPVLSVYVYPDDKYKETL	_
				CACTCGCTGTGGCCGCAGATCAAAGGGCGG	QLVDSTTSYGLTGAVFSQDKD	
				CIGCTGGAGGAGCACAGTCGGATCAAAGTG	VVQEATKVLRNAAGNFYINDK	
	-			GGCGACCCTGCAGAGGATTTTGGGACCTTCT	STGSIVGQQPFGGARASGTN	
				TCTCTGCAGTGATTGATGCCAAGTCCTTTGC	DKPGGPHYILRWTSPQVIKET	
				CCGTATCAAGAAGTGGCTGGAGCACGCGCG	HKPLGDWSYAYMQ*	
				CTCCTCGCCCAGCCTCACCATCCTGGCTGGG		

			L	GGCAAGTGTGATGACTCCGTGGGCTACTTTG		
				TGGAGCCCTGCATCGTGGAGAGCAAGGACC		
				CGGCCTGTACTGTCTGTACGTCTACCCG		
				GACGACAAGTACAAGGAGACGCTGCAGCTG		
				GTTGACAGCACCAGCTATGGCCTCACGG		
				GGGCAGTGTTCTCCCAGGATAAGGACGTCGT		
				GCAGGAGGCCACAAAGGTGCTGAGGAATGC		
				TGCCGGCAACTTCTACATCAACGACAAGTCC		
				ACTGGCTCGATAGTGGGCCAGCAGCCCTTTG		
				GGGGGCCCGAGCCTCTGGAACCAATGACA		
				AGCCAGGGGCCCACACTACATCCTGCGCT		_
	-			GGACGTCGCCGCAGGTCATCAAGGAGACAC		
				ATAAGCCCCTGGGGGACTGGAGCTACGCGT		
				ACATGCAGTGA		
Shigella 6	9	prey67711	184	AACAGAGCTGCCTCCTGGCTCTTTGGGAGCC	385	NRAASWI EGSI GGEGACBCA
ipaH9.8						AGKPPANSI AAAPPETASKUG
				GCGGGGAAGCCACCTGCGGATTCACTGGCT		GI PDI GI PAPCVRI GKPPSAD
				GCTGCTCCGCCCAGGACTGCTAGCAAGCAC		DPDPGPAWRKI
				GGAGGGCTGCCAGACCTGGGGCTCCCTGCT		
				CCGTGCGTCAGGTTGGGGAAACCACCGTCT		
				GCCCCAGACCCTGACCCAGGACCCGCCTGG		
Shigella 6		prey2118	182	ATGTCTCAGGCTGTGCAGACAAACGGAACTC	386	MSQAVQTNGTOPLSKTWELS
рану.о				AACCATTAAGCAAAACATGGGAACTCAGTTTA		LYELORTPOEAITDGLEIVVSP
				TATGAGTTACAACGAACACCTCAGGAGGCAA		RSLHSELMCPICLDMLKNTMT
				TAACAGATGGCTTAGAAATTGTGGTTTCACCT		TKECLHRFCADCIITALRSGNK
				CGAAGTCTACACAGTGAATTAATGTGCCCAAT		ECPTCRKKLVSKRSI RPDPNF
				TTGTTTGGATATGTTGAAGAACACCATGACTA		DALISKIYPSRDEYFAHOFRVI
				CAAAGGAGTGTTTACATCGTTTTTGTGCAGAC		ARINKHNNOOALSHSIEEGI KI
				TGCATCATCACAGCCCTTAGAAGTGGCAACA		QAMNRLORGKKOOIENGSGA
	-			AAGAATGTCCTACCTGTCGGAAAAAACTAGTT		EDNGDSSHCSNASTHSNOEA
				TCCAAAAGATCACTAAGGCCAGACCCAAACT		GPSNKRTKTSDDSGLELDNN
				TTGATGCACTCATCAGCAAAATTTATCCAAGT		NAAMAIDPVMDGASEIELVFR
				CGTGATGAGTATGAAGCTCATCAAGAGAGAG		PHPTLMEKDDSAQTRYIKTSG

			TATTAGCCAGGATTAGAGGAGGAC CAAGCACTCAGTCACCAGCATTAGAGAGGAC TGAAGATACAGGCCATGAACAGCACTGAGGAGGAC TGAAGATACAGGCCATGAACAGACTGCAGCG AGGCAAGAACAGATTGAACAGTTCACACT GGAGCAGAAGATAATGGTGACATCAGGA AGCAGCATCTGGCATCAGAATAATAATGATCAGATCA		NATVDHLSKYLAVRLALEELR SKGESNQMNLDTASEKQYTIY IATASGQFTVLNGSFSLELVSE KYWKVNKPMELYYAPTKEHK*
Shigella 6	prey3596	186	ATGTCCAAGCGGCACCGGTTGGACCTAGGG ATGTCCAAGCGGCACCGGTTGGACCTAGGG GAGGATTACCCCTCTGGCAAGAAGCGTGCG GGGACCGATGGAAGGATCGAGATCGAGAC CGGGATCGTGAAGGATCGGTCTAAAGATCGAG ACCGAGAACGTGATAGAGAAAGGAAGGAGT TGCGAGATTACCACCTCAAAGGAAGGAGT GCTGGATTACCACCCTCAAAGCATTCAGT GCTGGATTACCACCACTCAGCATTCAGC GCATTCTACAACCACTCAGCATG CCGGACATGCATTCTGCACTTCCACATG CCGGACATGCATCACCACTCAACGCATG CTCCTCGATCATTCTGCAAAGGAAAACGTAAACGCATA	387	MSKRHRLDLGEDYPSGKKRA GTDGKDRDRDREDRSKDR DRERDRGDREREREKEKEE LRASTNAMLISAGLPPLKASHS AHSTHSAHSTHSAHSTHA GHAGHTSLPQCINPFTNLPHT PRYYDILKKRLQLPVWEYKDR FTDILGRHQSFVLVGETGSGK TTQIPHRCVEYMRSLPGPKRG VACTQPRRVAAMSVAQRVAD EMDVMLGQEVGYSIRFEDCS SAKTFFMYMTDGMLLREAMN DPLLERYGVIILDEAHERTLAT DIN MCWLYGGENGON

187	/ I188 GATGACCACGCTATACACCGCCAAGAAGTAC 389 MTTLYTAKKYAVPAI FAHCVF
prey666	prey3917
Shigella ipa H9.8	Shigella 7 ospG

				CTTCGATGAACCGCAGCTGGCCAGCCTGTGC CTGGAGAAAAAAAAAA		IREVRLFNAVVRWSEAECQRQ QLQVTPENRRKVLGKALGLIR
_				CCATCACCGCGGAGGGCTTCACCGACATTGA		FPLMTIEEFAAGPAQSGILVDR
				CCTGGACACGCTGGTGGCTGTCCTGGAGCG		EVVSLFLHFTVNPKPRVEFIDR
				CGACACACTGGGCATCCGTGAGGTGCGGCT		PRCCLRGKECSINRFQQVESR
				GTTCAATGCCGTTGTCCGCTGGTCCGAGGCC		WGYSGTSDRIRFSVNKRIFVV
				GAGTGTCAGCGGCAGCAGCTGCAGGTGACG		GFGLYGSIHGPTDYQVNIQIIH
				CCAGAGAACAGGCGGAAGGTTCTGGGCCAAG		TDSNTVLGQNDTGFSCDGSA
				GCCCTGGGCCTCATTCGCTTCCCGCTCATGA		STFRVMFKEPVEVLPNVNYTA
				CCATCGAGGAGTTCGCTGCAGGTCCCGCAC		CATLKGPDSHYGTKGLRKVTH
				AGTCGGCCATCCTGGTGGACCGCGAGGTGG		ESPTTGAKTCFTFCYAAGNNN
				TCAGCCTCTTCCTGCACTTCACCGTCAACCC		GTSVEDGQIPEVIFYT*
				CAAGCCACGAGTGGAGTTCATTGACCGGCCC		
				CGCTGCTGCGTGGGAAGGAGTGCAGC		
				ATCAACCGCTTCCAGCAGGTGGAGAGTCGCT		
				GGGGCTACAGCGGGACCAGTGACCGCATCA		
				GETTCTCAGTCAACAAGCGCATCTTCGTGGT		
				GGGATTTGGGCTGTATGGATCCATCCACGGG		
				CCCACCGACTACCAAGTGAACATCCAGATTA		
				TTCACACCGATAGCAACACCGTCTTGGGCCA		
				GAACGACACGGGCTTCAGCTGCGACGGCTC		
				AGCCAGCACCTTCCGCGTCATGTTCAAGGAG		
				CCGGTGGAGGTGCTGCCCAACGTCAACTACA		
				CGGCCTGTGCCACGCTCAAGGGCCCCAGACT		
				CCCACTACGGCACCAAAGGCCTGCGCAAGG		
				TGACACACGAGTCGCCCACCGGGCGCCCA		
				AGACCTGCTTCACCTTTTGCTACGCGGCCGG		
				GAACAACAATGGCACATCCGTGGAGGACGG		
Shigella	7	prey63632	189		390	CGKAFSWKSHLIEHQRTHTGE
osbe				CTTATTGAGCATCAAGAACTCACACTGGTGA		KPYHCTKCKKSFSRNSLLVEH
				GAAACCTTATCACTGTACCAAATGTAAGAAGA		QRIHTGERPHKCGECGKAFRL
				GCTTTAGTCGAAATTCATTGCTTGTTGAGCAT	•	STYLIQHQKIHTGEKPFLCIEC
				CAAAGAATTCACACTGGGGAAAGACCCCATA		GKSFSRSSFLIEHORIHTGERP
				AATGTGGTGAATGTGGGAAAGCCTTTCGATT		YQCKECGKSFSQLCNLTRHQ

			_	AAGCACATACCTTATACAACACCAAAAAATTC		RIHTGUKPHKCEECGKAESBS
				ACACTGGCGAGAGCCTTTTCTTTGTATTGAG		SGLIQHQRIHTREKTYPYNETK
				TGTGGAAAAGTTTCAGTCGGAGCTCATTCC		ESFDPNCSLVIQQEVYPKEKS
				TTATTGAACATCAGAGGATCCATACTGGTGAA		YKCDECGKTFSVSAHLVQHQ
				AGACCTTATCAGTGCAAAGAGTGTGGGAAAA		RIHTGEKPYLCTVCGKSFSRS
				GTTTCAGTCAGCTTTGCAACCTTACTCGTCAT		SFLIEHQRIHTGERPYLCRQC
				CAGAGAATTCACACAGGAGACAAGCCCCATA		GKSFSQLCNLIRHQGVHTGNK
				AATGTGAGGAATGTGGAAAAGCCTTTAGTAG		PHKCDECGKAFSRNSGLIOHO
				AAGCTCAGGTCTTATTCAGCATCAGAGAATTC	-	RIHTGEKPYKCEKCDKSFSOO
				ACACCAGGGAGAGACTTATCCATACAATGA		RSLVNHOMIHAEVKTOETHEC
				AACTAAGGAAAGTTTTGATCCAAATTGCAGTC		DACGEAFNCRISLIOHOKLHTA
				TTGTTATACAGCAGGAAGTCTACCCTAAGGA		WMO*
				GAAATCTTATAAATGTGATGAATGTGGGAAAA		
				CTTTTAGTGTTAGTGCTCATCTTGTACAACAT		
				CAAAGAATCCACACTGGTGAAAAGCCCTATC		
				TATGTACTGTCTGTGGGAAGAGCTTCAGCCG		
				GAGCTCATTTCTTATTGAACATCAGAGAATCC		
				ACACTGGAGAGACCCTATCTGTGCAGACA		
				GTGTGGAAAAGCTTTAGTCAGCTTTGTAATC		
				TTATTCGACATCAGGGTGTTCACACAGGTAAT		
				AAACCCCATAAATGTGATGAATGTGGAAAGG		
				CCTTTAGCCGGAACTCGGGTCTTATTCAGCA		
				TCAGAGAATACACACAGGAGAGAAACCTTAT		
		-		AAGTGTGAGAAGTGCGACAAAAGTTTCAGTC		
				AACAGCGCAGTCTTGTCAACCATCAGATGAT		
				CCATGCAGAGGTGAAAACCCAAGAAACCCAT		
				GAATGTGATGCTTGTGGTGAAGCCTTTAATTG		
				CCGTATTCTCTTATTCAGCATCAGAAATTGC		
				-		
Shigella	_	prey2109	190		391	TKDHHYFKYCKISALALLKMV
osbe				AAATCTCAGCATTGGCTCTTCTGAAGATGGT		MHARSGGNLEVMGLMLGKVD
				GATGCATGCCAGATCGGGAGGCAATTTGGAA		GETMIIMDSFALPVEGTETRVN
				GTGATGGGTCTGATGCTAGGAAAGGTGGATG		AQAAAYEYMAAYIENAKQVGR
				GTGAAACCATGATCATTATGGACAGTTTTGCT		LENAIGWYHSHPGYGCWLSGI
				TTGCCTGTGGAGGGCACTGAAACCCGAGTAA		DVSTOMLNOOFOEPFVAVVID

2	392	GGCCAAGCCG 393 TGAAPAKAKPAEAPAAAAPKA GCCCCAAAAG GCCCCAAAAG STTCCTCCCCC GATGCCACCG GATGCCACCG CCTTCTGGCA FNACTICTGCA FNACTICTGCA FNACTICTGCAA FNACTIC
TGCATACATAGAAATGCAAAACAGTTGGC CGCCTTGAAAATGCAATCGGGTGGTTGATA GCCACCCTGGCTATGGCTGCTGGCTTTCTGG GATTGATGTTGTAGGTTGCTGCTGCTTTTTGG GATTGATGTTGTAGCTTTGTAGGTGGTGTTTTGG AGTTCCAGAACCATTTGTAGGACATACCCAA GGGATCTTGGCGCCTTTAGGACATACCCAA AGGCTACAAACCTCCTGATGAAGGACCTTC TGAGTACCAGACTATTCCACTTAATAAAATAG AAGATTTTGGTGTACACTGCAAACAATATTT GGGTTAGAAATTGCTTGAAAATATAAAATAT GGGTTAGAAATTGCTTGAAAATTAT GGGTTAGAAATTGCTTGAAATCCTCTTT	CGTGACCTCCAGCATGTTGTTGTTGGCAGGTC CGTGACCCTCCAGCATGTTCATTGGCAGGTC CAGTTGGGGATGATGTTTCATTGGCAGGTC CACAATTATGGGACCTAATGACAGTTCATTT CCAGAGTGTTTCTTTTTGACAATTCATTT TCCTACAGACTACCCCTTCAAACCACATA TTCTAAGATTACAACAGAATTTATCATCCAAA TATTAACAGTATGGCAGCATTTGTCTCGATA TTCTAAGATCAAGGCGCATTTGTTCACAA ATTTCTAAAGTTCTTTTATCCATTTGTTCACAG CTATGTGATCCAAACCCAGATGACCCCTAG TGCCAGAGATTGCAAAACAGA CAGAGATTGCAAAAACAGA CAGAGATTGCAAGAACCCAGATGTGAAAAACAGA CAGAGATAGCAACAGAATTCTCGGGAA TGCCAGAAGTTCTTAAAAACAGA	AACTIGGTGCTCCTGCTAAGGCCAAGCCG GCTGAAGCTCCTGCTGCTGCAGCCCAAAAG GCTGAAGCTACAGCAGCCCAAAAG CAGAACCTACAGCAGCGCAGTTCCTCCCCC TGCAGCACCCATACCCACTCAGATGCCACCG GTGCCCTCACAGCCCCTCTCTGGCA AACCTGTGTCTGCACAAAACCCACTGTTGC
		78 <u>-</u>
100 E 4004		prey 1922
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Chirollo	ospG	ospo Ospo

		L	AACAGGATGCGCACCCATTCCTCACCT			ſ
		 -	CTGAAGGAGCCCAGAATACATGTGCAATGC		VEAMNEADIEDTITEL CEVABO	
-			TGACAACTTTTAATGAGATTGACATGAGTAAC		NEI AIEDMOGATETISNGGVE	٠.,
			ATCCAGGAGATGAGGGCTCGGCACAAAGAG		GSLEGTPIINPPOSAII GMHGIE	ш
			GCTTTTTGAAGAACATAACCTCAAACTAGG		DRPVAIGGKVFVRPMMYVAI T	
			CTTCATGTCGGCATTTGTGAAGGCCTCAGCC		YDHRLIDGREAVTEI RKIKAAV	- >
			TTTGCCTTGCAGGAACAGCCTGTTGTAAATG		EDPRVLLLDL*	
_			CAGTGATTGACGACACCAAAGAGGTGGT			
_			GTATAGGGATTATATTGACATCAGTGTTGCAG			
			TGGCCACCCCACGGGGTCTGGTGGTTCCAG			
			TCATCAGGAATGTGGAAGCTATGAATTTTGCA			
			GATATTGAACGGACCATCACTGAACTGGGAG			
			AGAAGGCCCGAAAGAATGAACTTGCCATTGA			
			AGATATGGATGGCGGTACCTTCACCATTAGC			
			AATGGAGGCGTTTTTGGCTCGCTCTTTGGAA			
7.			CACCCATTATCAACCCCCTCAGTCTGCCAT			
			CCTGGGGATGCATGCATCTTTGACAGGCCA			
			GTGGCTATAGGAGGCAAGGTAGAGGTGCGG			
			CCCATGATGTACGTGGCACTGACCTATGATC			
			ACCGGCTGATTGATGGCAGAGGCTGTGA			
			CTTTCCTCCGCAAAATCAAGGCAGCGGTAGA			
Shigella 7	prey67418	193			AASRRLMKEL EFIRKCGMKNE	٦.
			TGAAGAAATCCGCAAATGTGGGATGAAAAAC		RNIQVDEANLLTWOGLIVPDN	
			TTCCGTAACATCCAGGTTGATGAAGCTAATTT		PPYDKGAFRIEINFPAEYPFKP	_
			ATTGACTTGGCAAGGGCTTATTGTTCCTGACA		PKITEKTKIYHPNIDEKGOVCI	
			ACCCTCCATATGATAAGGGAGCCTTCAGAAT		PVISAENWKPATKTDQVIQSLI	
			CGAAATCAACTTTCCAGCAGAGTACCCATTCA		AL VNDPOPEHPI RADI AFEYS	
			AACCACCGAAGATCACATTTAAAACAAAGATC		KDRKKFCKNAFFFTKKYGEKB	
			TATCACCCAAACATCGACGAAAAGGGGCAGG		PVD*	
			TCTGTCTGCCAGTAATTAGTGCCGAAAACTG			
	_		GAAGCCAGCAACCAAACCGACCAAGTAATC	**		
			CAGTCCCTCATAGCACTGGTGAATGACCCCC			
			AGCCTGAGCACCCGCTTCGGGCTGACCTAG	•		
			CTGAAGAATACTCTAAGGACCGTAAAAAATTC			

AGAAATA A	MASMRVVKELEDLOKKPPP CCCCCAT CCCCCAT ATGCCAA CCTACCC CCTACC CCTACC CCTACC CCTACC CCTACC CCTACC CCTACC CCTACC CCTACC CCCCACC CCCCACC CCCCCACC CCCCCACC CCCCCC	GAGAGC 396 MSVGHKAQESKIRYKTNEPV CTGTGTG CACAATC CACAATC AGGTCAG SGGGAA GCTCACC CGCTTCC SCACCAT SACCCAT	397
TYP V CHICATAL	MMASMKVVAE YLRNLSSDDAN DQPPYHLKAFN KPPMIKFTTKIYI CLPIISSENWKF LNVLVNRPNIRE TQNPELFRKNA RPS*	MSVGHKAQESK WEENFTFIHNI RDEQHQCSLGN SEDMTVSQRFG KMKIALRVLHLE	WDALKAAAYAAEANDHELAQ AILDGASITLPHGTLCECYDEL GNRYQLPIYCLSPPVNLLLEHT EEESLEPPEPPPSVRREFPLK VRLSTGKDVRLSASLPDTVGC LKRQLHAQEGIEPSWQRWFF SGKLTDRTRLQETKIOKDFVI
	362	396	397
IGTAAGAATGCTGAAGAGTTTACAAAGAAATA TGGGGAAAAGCGACCTGTGGACTAA			CTGGGATGCCCTCAAGGCTGCCGCCTATGCT GCTGAAGCCAACGACCACGAGCTGGCCCAG GCCATCCTGGATGGAGCCAGCATCACCCTGC CTCATGGCACCCTCTGTGAATGCTACGATGA GCTGGCCATCGCTACCACCATCAC TGCCTGTCACCAGCTGCCCATCTAC TGCCTGTCACCGGTGAACCTGCTGC GAGCACGCGGGGAAGCCTGGAGCCC
	194	195	196
	prey67314	prey67435	prey67443
	~	_	<u> </u>
	Shigella ospG	Spigella ospG	Shigella ospG

				TTCCCGCTGAAGGTGCGCCTGTCCACGGGC AAGGACGTGAGGCTCAGCGCCCGCCC GACACAGTGGGCCTCAGCGCCCAGCCTGCC GACACAGTGGGCCAGCTCAGGGCAGCTG CACGCCCAGGAGGCATCGAGCCATCGTGG CAGCGGTGGTTCTTCTCCGGGAAGCTGCTCA CAGACCGCACAGGGCTCCAGGAGCCACAGA TCCAGAAAGATTTTGTCATCCAGGGTCATCATC AAC		
Shigella ospG	2	prey67317	197	() (0 (0 ()	398	SVPSAARSSSAPSGCAPTSKR CTGLPRRPWSSPVPSTRASA SWNLVGTSSKKLWGTSYSW WKRSLPSRA*
Shigella ospG	۲	prey67393	198	GAGAATCCACAAGGAATTGAATGATCTGGCA CGGGACCCTCCAGCAGTGTTCAGCAGGT CGGGACCTCCAGCAGTGTTCAGCAGGT CCTGTTGGAGATGATGTTCCATTGCCAGG CTACAATAATGGGGCCAAATGACAGT TCAGGGTGGAGTATTTTTCTTGACAATTCATT TCCCAACAGATTACCCCTTCAAACCACAA TATTACAACAGAATTATCATGATA TTTAACAGTAATGGCAGCATTTGTCTTGATA TTTAACAGTAATGGCAGCATTTGTCTTGATA TTTCACGATCACAGCATTTGTCTTTAC ATTTCAAAAGTACTCTTGTCCATCTTTAG TGCTGAGATTGCTCGGATCTTAG TGCTGAGATTGCTCGGAAATAGCTCGGGAA TGGACTCAGAAGAATAGCTCGGGAA	399	RIHKELNDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPY QGGVFLTIHFPTDYPFKPPKV AFTTRYHPNINSNGSICLDILR SQWSPALTISKVLLSICSLLCD PNPDDPLVPEIARIYKTDREKY NRIAREWTQKYAM*
Shigella ospG	۲	prey700	199	ATGGGAATTGGTCTTTCTGCTCAAGGTGTGA 4 ACATGAATAGACTACCAGGTTGGGATAAGCA TTCATATGGTTACCATGGGGATGATGGACATT CGTTTTGTTCTTCTGGAACTGGACACCTTAT GGACCAACTTTCACTACTGGTGATGTCATTG	400	MGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQ PYGPTFTTGDVIGCCVNLINNT CFYTKNGHSLGIAFTDLPPNLY PTVGLQTPGEVVDANFGQHP FVFDIEDYMREWRTKIQAQID

				TOTTACACCAAGAATGGACATAGTTTAGGTAT TGCTTTCACTGACCTACGCCCAAATTTGTATC		RFPIGDREGEWQTMIQKMVS SYLVHHGYCATAEAFARSTDQ
				GGTCGATGCCAATTTTGGGCAACATCCTTTC GTGTTTGATATAGAAGACTATATGCGGGAGGT		I VLEELASIKNRÜRIÜKLVLAG RMGEAIETTQ
				GGAGAACCAAAATCCAGGCACAGATAGATCG		
				ATTTCCTATCGGAGATCGAGAGGAGGAGTGG		
				TTTAGTCCACCATGGGTACTGTGCCACAGCA		
				GAGGCCTTTGCCAGATCTACAGACCG		
				CANACANTECACANTAGE TENERAL TENERAL CONTROLL OF THE CONTROLL OF		
				GAATGGGAGAAGCCATTGAAACAACACAAC		
Shigella	7	prey67411	200	-	401	PEEGEERKPSATQQKKNTKLS
osbG				GCCACCCAGCAGAAAAAACACCCAAACTCT		SKTTAKLSTSAKRIQKELAEITL
				CTAGCAAAACCACTGCTAAGTTATCCACTAGT	-	DPPPNCSAGPKGDNIYEWRS
				GCTAAAAGAATTCAGAAGGAGCTAGCTGAAA		TILGPPGSVYEGGVFFLDITFS
				TAACCCTTGATCCTCCTCCTAATTGCAGTGCT		SDYPFKPPKVTFRTRIYHCNIN
				GGGCCTAAAGGAGATAACATTTATGAATGGA		SQGVICLDILKDNWSPALTISK
- N				GATCAACTATACTTGGTCCACCGGGTTCTGT		VLLSICSLLTDCNPADPLVGSI
				ATATGAAGGTGGTGTTTTTTTCTGGATATCA		ATQYLTNRAEHDRIARQWTKR
	_			CATTTCATCAGATTATCCATTTAAGCCACCA		YAT*
	-			AAGGTTACTTTCCGCACCAGAATCTATCACTG		
				CAACATCAACAGTCAGGGAGTCATCTGTCTG		
				GACATCCTTAAAGACAACTGGAGTCCCGCTT		
				IGACIAI II CAAAGGII II IGCI GI CI AII I GTI		
				CCCTTTTGACAGACTGCAACCCTGCGGATCC		
				TCTGGTTGGAAGCATAGCCACTCAGTATTG		
				ACCAACAGAGCAGAACACGACAGGATAGCCA		
Shigella	7	prey67423	201	ATGAGTTCTCAACAGTTTCCTCGGTTAGGAG	402	MSSQQFPRLGAPSTGLSQAP
osbG				CCCCTTCTACCGGGCTGAGCCAGGCCCCTTC		SQIANSGSAGLINPAATVNDES
				TCAGATTGCAAACAGTGGTTCTGCTGGATTG		GRDSEVSAREHMSSSSSLQS
				ATAAACCCAGCTGCTACAGTCAATGATGATC		REEKQEPVVVRPYPQVQMLS
				TGGTCGAGATTCTGAAGTCAGTGCCAGGGAG		THHAVASATPVAVTAPPAHLT

				CACATGAGTTCCAGCAGCTCCCTCCAGTCCC GGGAGGAGGAAGCAGAGCCTGTTGTGGTAA		PAVPLSFSEGLMKPPPKPTMP SRPIAPAPPSTLSLPPKVPGQV
				GGCCCTATCCACAGGTGCAGATGTTGTCGAC		TVTMESSIPQASAIPVATISGQ QGHPSNLHHIMTTNVQMSIIRS
				GCAGTGACAGCCCCGCCAGCACCTGACG		NAPGPPLHIGASHLPRGAAAA
				CCAGCAGTGCCACTTTCATTTTCGGAGGGAC		AVMSSSKVTTVLRPTSQLPNA
				TTATGAAGCCGCCCCGAAGCCCACCATGCC		ATAQPAVQHIIH
				TAGCCGTCCCATTGCTCCTGCTCCACCTTCT		
				ACCCTGTCACTTCCCCCCAAGGTTCCAGGGC		
				AGGTTACCGTTACCATGGAGAGTAGCATCCC		
				TCAAGCTTCAGCCATTCCTGTGGCAACAATC		
				AGTGGACAACAGGGCCATCCCAGTAACCTGC		
				ATCACATCATGACTACAAATGTGCAAATGTCT		
				ATCATCCGCAGCAATGCTCCTGGGCCCCCTC		
				TTCACATTGGAGCTTCTCATTTACCTCGAGGT		
				GCAGCTGCTGCTGTGATGTCCAGTTCTA		
				AAGTAACCACAGTCCTGAGGCCGACCTCACA		
				GCTGCCAAATGCTGCTACTGCTCAGCCAGCA		
				GTACAGCACATCATCACC		
higella	7	prey67298	202	GATATTCTAGGTGTTAGGGTGCTGCAATCCC	403	DILGVRVLQSPGTVLVDFIS*V
osbG				CTGGAACTGTATTAGTTGATTTTATTTCATGA		CIKHLLSMGLAWGLVLXTYR*T
				GTGTGCATAAAACACCTTCTATCTATGGGACT		RSLLARS*ELSEERVKSPQ*EH
				GGCATGGGCTTGGTGCTTANAACATATAGA		GGAHTWAAGTLPXPDPVLTLK
				TGAACAAGATCTTTGCTAGCAAGGAGCTGAG		NVXMIXRXG
				AGCTTAGTGAAGAAGAGTGAAAAGTCCACA		
				GTGAGAACATGGAGGNGCACATACCTGGGC		
				TGCAGGCACACTGCCTNTGCCTGATCCAGTC		
				CTGACACTGAAAATGTGNNCATGATANGAA		
				GANGGGGG		
Shigella		prey67464	203	NTTGNTGGGTGNGNTNGGGGTGATAAGGAA	404	XXGXXXGDKERV*ENGIKQGT
osbG				AGAGTGTGAGAAATGGCATCAAACAGGGAA		SKRSGGKRTRDESVNPHN*DL
				CAAGTAAGAGGTCTGGTGGCAAGCGGACAA		RGMSGS*ELRQS*VGGPTIN*K
				GAGATGAGTCCGTCAACCCCCACAACTGAGA		RDQLTCYXXSYPGLRCXDGS
				CTTGAGAGGGATGAGTGGGTCCTGAGAACTC		GGRXPXPXGPGLXXXE
				AGGCAAAGC1GAG1AGG1GGCCCCAC1A1CA		

				ATTAAAAAGAGATCAGCTTACCTGCTACTAN TANAGTTACCCTGGGCTCCGATGCANTGATG GCAGTGGGGGCCGGNAGCCGGNGCCCANG GCACTGGCCTNATNANTNTTGAG		
Shigella ospG	2	prey67320	204		405	SVPARYFDKLARTALFRWSIE HRDYFSSPWQLSTDLCLPSLK YIYF*TMYAI*FISVIVVGDLIDII WLCVLPC*QVIYVSKFLPSGN* VSLIL
Shigella ospG	2	prey67321	205	∠ ∟⊢	406	VLSXLRXXVAIEXLXQEP*KDV XSXXXSKXAGGXPXYHXGAF XXXLSXRAFLFQLXXHMEVVTI XSLQYYXHQNXFLQXXLVVXX XXWXLDXAEXVXGGX
Shigella ospG	_	prey35777	206	ATGGGGCCCTCTCAGCCCCTCCCTGCACA GAGCACATCAAATGGAAGGGGCTCCTGGTCA CAGCATCACTTTTAAACTTCTGGAACCTGCCC ACCACTGCCCAAGTCACGATTGAAGCCTGCCC ACCACTGCCCAAGTCACGATTGAAGCCCAGC CACCAAGTTTCCGAGGGGAAGGATGTTC TCTACTTGTCCACATTTGCCCCAGAATCTTA CTGCTTACCACAATTTGCCCCAGAATCTTA TCTACTTGTCCACAATTACATTAC	407	MGPLSAPPCTEHIKWKGLLVT ASLLNFWNLPTTAQVTIEAQP PKVSEGKDVLLLVHNLPQNLT GYIWYKGQIRDLYHYITSYVVD GQIIIYGPAYSGRETAYSNASL LIQNVTREDAGSYTLHIIKRGD GTRGVTGYFTFTLYLETPKPSI SSSNLNPREAMETVILTCDPE TPDTSYQWWMNGQSLPMTH RFQLSETNRTLFLFGVTKYTA GPYECEIRNSGSASRSDPVTL NILHGPDLPRIHPSYTNYRSG

DNLYLSCFANSNPPAGYSW II NGKFQQSGQNLFIPQITTKHS GLYVCSVRNSATGQESSTSLT VKVSASTRIGLLPLLNPT*	QALNFTRFLDQSGPPSGDVN SLDKKLVLAFRHLKLPTEWNV LGTDQSLHDAGPRETLMHFAV RLGLLRLTWFLLQKPGGRRAL SIHNQEGATPVSLALERGYHK LHQLLTEENAGEPDSWSSLSY EIPYGDCSVRHHRELDIYTLTS ESDSHHEHPFPGDGCTGPIFK LMNIQQQLMKTNLKQMDSLM PLMMTAQDPSSAPETDGQFL PCAPEPTDPQRLSSSEETEST QCCPGS
	804
AAGCGAGGTGATGGGACTAGAGGAGTAACT GGATATTTCACCTTCACCTTATACCTGGAGAC TCCCAAGCCCTCCATCTCCAGCAGCACTTA AACCCCAGGGAGGCCATGGAAACTGTGATCT TAACCTGTGATCCTGAGACTCCGGACACAG CTACCAGTGGTGGATGATTGGTCAGAGCCTC CCTACGACAGGACCCTTTCTATTTGGTGTCAGAA AAGTATACTGCAGGACCCTATTTTTGGTGTCACA AAGTATACTGCAGGACTCCTATTTTTTTGGTGTCACA ACGGAACTCAGGAGTTCCTCCTTTTTTGGTGAAT ACGGAACTCAGGAGTTCCTCCATGGTCACA ATTACCGTTCAGGAGTAATCACCCTCATGGTCC TCACAAAGCATTAATGGGAAGTTTCAGCAA TCACAAAGCATTAATGGGAAGTTTCACTTGCT TCACAAAGCATTAATGGGAAGTTTCAGCAA TCACAAAGCATAATGGGCACAATTAC CCACATCGTAACTCATGGTTTGCTCT GTTCGTAACTCAGGCAAGTCTCTCAAACC CCACATCGTTGACTCTCTCTCTCTCTAATCC ACAAGAATAGGACTTCTTCCTTCTCTAATCC ACAACAATAGGACTTCTTCCTTCTCTAATCC	GCAGGCTTTGAACTTTACCCGTTTTCTTGACC GCAGGCTTTGAACACTTGGGGGATGTGAACTTGGGGGATGTGGAATTC CCTTGATAAGAAGTTGGTGCTGGCATTCAGG CCCCGAAGAGTTGGCATGTGATGTAT TGGGGACAGATCAGAGTTTGCATGTTTTGCTGG CCGCGAGACATTGATGCATTTTGCTGTG CCGCGAGAGCCTGGAGTTGATGCTGGGCTGG
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	Shigella ospG

				TTAACCTCTGAGTCTGATTCACATCATGAGCA	
	_,			CCCATTTCCTGGAGACGGTTGCACTGGACCA	
				ATTTTAAACTTATGAACATCCAACAGCAACI	
				AATGAAAACAAACCTCAAGCAGATGGACAGT	
				CTTATGCCCTTAATGATGACAGCACAGGATC	
				CTTCCAGTGCCCCAGAGACAGATGGCCAGTT	
				TCTTCCCTGTGCACCGGAGCCCACGGACCCT	
				CAGCGACTTTCTTCTGAAGAGACTGAGA	
				GCACTCAGTGCTGCCCAGGGAGCCC	
Shigella	7	prev412	208	t	SIAPKTTRVTYPAKAKGTFIAD
Saso				TACCCAGCCAAAGCCAAGGGCACATTCATCG	SHQNFALFFQLVDMNTGAELT
)				CAGACAGCCACCAGAACTTCGCCTTGTTCTT	PHQTFVRLHNQKTGQEVVFV
				CCAGCTGGTAGATATGAACACTGGTGCTGAA	AEPDNKNVYKFELDTSERKIEF
				CTCACTCCTCACCAGACATTTGTCCGACTCC	DSASGTYTLYLIIGDATLKNPIL
				ATAACCAGAAGACTGGCCAGGAAGTGGTT	WNVADVVIKFPEEEAPSTVLS
				TGTTGCCGAGCCAGACAACAAGAACGTGTAC	QNLFTPKQEIQHLFREPEKRP
	-			AAGTTTGAACTGGATACCTCTGAAAGAAAGAT	PT
				TGAATTTGACTCTGCCTCTGGCACCTACACTC	
	_			TCTACTTAATCATTGGAGATGCCACTTTGAAG	
				AACCCAATCCTCTGGAATGTGGCTGATGTGG	
				TCATCAAGTTCCCTGAGGAAGAAGCTCCCTC	
				GACTGTCTTGTCCCAGAACCTTTTCACTCCAA	
				AACAGGAAATTCAGCACCTGTTCCGCGAGCC	
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Shinella	7	prev50598	209	Ť	LRVRSLPGEDLRARVSYRLLG
OsoG					VISLLHLVLSMGLQLYGFRQR
)				GGGGGTCATCTCACTGCTGCACCTGGTGCTG	QRARKEWRLHRGLSHRRASL
				TCCATGGGGCTGCAGCTGTACGGTTTCAGGC	EERAVSRNPLCTLCLEERRHP
				AGCGCCAGCCAGGAAGGAGTGGAGGC	TATPCGHLFCWECITAWCSSK
				TGCACCGCGCCTGTCTCACCGCAGGGCCT	AECPLCREKFPPQKLIYLRHY
				CCTTGGAGGGAGAGCCGTTTCCAGAAACCC	**
				cctgtgcaccctgtgcctggaggaggggag	
				GCACCCAACAGCCACGCCTGCGGCCACCT	
				GTTCTGCTGGGAGTGCATCACCGCGTGGTG	
				CAGCAGCAAGGCGGAGTGTCCCCTCTGCCG	

			GGAGAAGTTCCCTCCCCAGAAGCTCATCTAC		
I	prey67364	210	TTATTAAATGAAACAACAGTGGAAATATAGCC 411 AGACCTGACTAACCTTGCCTGTATTTCTTGT		LLNETTVEI*PDLTNLACIFL*AG ENQRHQDLVEGPVCCLTHTS POVPBGRHHRPI R*GEALIFG
			GGTAGAAGGCCGGTCTGCTTTAACACAT		ETEAAHCLYLEVENMXFCIYLC
			ACCAGCAGACAGG CCCACG GGGAGGCAC CACAGACCTTTAAGATAGGGTGAAGCCTTGA		LEAN I FAIN
			TAGAAGGAGAAACAGAGCTGCCCACTGTCT	_	
			TTACTTAGAAGTGGAGAACATGGNATTCTGTA TTTATTTATGTTGACTGCGCANCTTTACNTTT		
1	prey67367	211	ATCCAGCAAAACCGCTGCTAAATTGTCAACTA 412	2	SSKTAAKLSTSAKRIQKELAEI
			GTGCTAAAAGAATTCAGAAGGAACTTGCAGA		ILDPPPNCSAGPKGDNIYEWK
			COTOCACAL IGGACCOLOCOCACO GO I AGO I COTOCACO GO I COTOCAC		SPLYPEKPPKVTERTRIVHCNI
			GGAGGTCAACTATTGGGACCCCCAGGATC		NSOGVICLDILKDNWSPALTIS
			TGTCTATGAAGGAGGGGTGTTCTTCTTGAC		KVLLSICSLLTDCNPADPLVGS
			ATTACCTTTTCACCAGACTATCCGTTTAAACC		IATQYMTNRAEHDRMARQWT
			CCCTAAGGTTACCTTCCGAACAAGAATCTATC		KRYAT*
			ACTGTAATATTAACAGCCAAGGTGTGATCTGT		
			CTGGACATCTTAAAGGACAACTGGAGTCCGG	_	
			CTTTAACTATTTCTAAAGTTCTCCTCTCCATCT		
			GCTCACTTCTTACAGATTGCAACCCTGCTGA		
			CCCTCTGGTGGGCAGCATCGCCACACAGTAC		
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			GCCAGACAGTGGACCAAGCGGTACGCCACA		
	prey67369	212	+	3	VAMSRDGATHVYETHPWWNF
			TATATGAAACTCATGGTGGTGGAACTTTTT		FOMCELCALLESWKHSIFKS I
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			ATATCTCTATCAGGAAATTAAAATTGTTAGCTT		KEKIYETXLN
			ATATCTACATTTCAATAAAATGTAAGCCTGTT		
_			GCIAIGIIGAIAGCAAAICIGIIIAACIIACI		

CAAC GAGATAAGGTGATGTCAGAGTTTAATAACAAG
GAGALAAGGIGATGICAGAGITTAATAACAAC TTCCGGCAGCAGATGGAGAATTACCCGAAAA ACAACCACACTGCTTCGATCCTGGACAGGAT
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